FIG. 1A

```
                                                                GGCTGCCGG
                                                                     -120
AGGGGCGGCCGTGCGTGGATGCGGCGGGAGCTGGAAGCCTCGAGCAGCCGGCGCCTTCT
CTGGCCCCGGGCGCCATATGGCTTGAAGAGCCGTGCCACCCAGTGGCCCCACTGCCCCA
                                                              -1
 1              *                        10
Met Asp Pro Leu Asn Leu Ser Trp Tyr Asp Asp Asp Leu Glu Arg
ATG GAT CCA CTG AAC CTG TCC TGG TAC GAT GAC GAT CTG GAG AGG
1
     *          20          *                              30
Gln Asn Trp Ser Arg Pro Phe Asn Gly Ser Glu Gly Lys Ala Asp
CAG AAC TGG AGC CGG CCC TTC AAT GGG TCA GAA GGG AAG GCA GAC
                                                           90
                                       40
Arg Pro His Tyr Asn Tyr Tyr Ala Met Leu Leu Thr Leu Leu Ile
AGG CCC CAC TAC AAC TAC TAT GCC ATG CTG CTC ACC CTC CTC ATC

                50                                         60
Phe Ile Ile Val Phe Gly Asn Val Leu Val Cys Met Ala Val Ser
TTT ATC ATC GTC TTT GGC AAT GTG CTG GTG TGC ATG GCT GTA TCC
                                                          180
```

TOT280" 85E4E660

									70					
Arg	Glu	Lys	Ala	Leu	Gln	Thr	Thr	Thr	Asn	Tyr	Leu	Ile	Val	Ser
GCA	GAG	AAG	GCT	TTG	CAG	ACC	ACC	ACC	AAC	TAC	TTG	ATA	GTC	AGC
				80										90
Leu	Ala	Val	Ala	Asp	Leu	Leu	Val	Ala	Thr	Leu	Val	Met	Pro	Trp
CTT	GCT	GTG	GCT	GAT	CTT	CTG	GTG	GCC	ACA	CTG	GTA	ATG	CCG	TGG
														270
									100					
Val	Val	Tyr	Leu	Glu	Val	Val	Gly	Glu	Trp	Lys	Phe	Ser	Arg	Ile
GTT	GTC	TAC	CTG	GAG	GTG	GTG	GGT	GAG	TGG	AAA	TTC	AGC	AGG	ATT
				110										120
His	Cys	Asp	Ile	Phe	Val	Thr	Leu	Asp	Val	Met	Met	Cys	Thr	Ala
CAC	TGT	GAC	ATC	TTT	GTC	ACT	CTG	GAT	GTC	ATG	ATG	TGC	ACA	GCA
														360
									130					
Ser	Ile	Leu	Asn	Leu	Cys	Ala	Ile	Ser	Ile	Asp	Arg	Tyr	Thr	Ala
AGC	ATC	CTG	AAC	CTG	TGT	GCC	ATC	AGC	ATT	GAC	AGG	TAC	ACA	GCT
				140										150
Val	Ala	Met	Pro	Met	Leu	Tyr	Asn	Thr	Arg	Tyr	Ser	Ser	Lys	Arg
GTG	GCA	ATG	CCC	ATG	CTG	TAT	AAC	ACA	CGC	TAC	AGC	TCC	AAG	CGC
														450

FIG. 1B

09934358.082101

									160					
Arg	Val	Thr	Val	Met	Ile	Ala	Ile	Val	Trp	Val	Leu	Ser	Phe	Thr
CGA	GTT	ACT	GTC	ATG	ATT	GCC	ATT	GTC	TGG	GTC	CTG	TCC	TTC	ACC
				170										180
Ile	Ser	Cys	Pro	Leu	Leu	Phe	Gly	Leu	Asn	Asn	Thr	Asp	Gln	Asn
ATC	TCC	TGC	CCA	CTG	CTC	TTC	GGA	CTC	AAC	AAT	ACA	GAC	CAG	AAT
														540
									190					
Glu	Cys	Ile	Ile	Ala	Asn	Pro	Ala	Phe	Val	Val	Tyr	Ser	Ser	Ile
GAG	TGT	ATC	ATT	GCC	AAC	CCT	GCC	TTT	GTG	GTC	TAC	TCC	TCC	ATT
				200										210
Val	Ser	Phe	Tyr	Val	Pro	Phe	Ile	Val	Thr	Leu	Leu	Val	Tyr	Ile
GTC	TCA	TTC	TAC	GTG	CCC	TTC	ATC	GTC	ACT	CTG	CTG	GTC	TAT	ATC
														630
									220					
Lys	Ile	Tyr	Ile	Val	Leu	Arg	Lys	Arg	Arg	Lys	Arg	Val	Asn	Thr
AAA	ATC	TAC	ATC	GTC	CTC	CGG	AAG	CGC	CGG	AAG	CGG	GTC	AAC	ACC
				230										240
Lys	Arg	Ser	Ser	Arg	Ala	Phe	Arg	Ala	Asn	Leu	Lys	Thr	Pro	Leu
AAG	CGC	AGC	AGT	CGA	GCT	TTC	AGA	GCC	AAC	CTG	AAG	ACA	CCA	CTC
														720

FIG. 1C

09934358.082101

```
                                                  250
Lys Asp Ala Ala Arg Arg Ala Gln Glu Leu Glu Met Glu Met Leu
AAG GAT GCT GCC CGC CGA GCT CAG GAG CTG GAA ATG GAG ATG CTG

                260                                     270
Ser Ser Thr Ser Pro Pro Glu Arg Thr Arg Tyr Ser Pro Ile Pro
TCA AGC ACC AGC CCC CCA GAG AGG ACC CGG TAT AGC CCC ATC CCT
                                                        810
                                      280
Pro Ser His His Gln Leu Thr Leu Pro Asp Pro Ser His His Gly
CCC AGT CAC CAC CAG CTC ACT CTC CCT GAT CCA TCC CAC CAC GGC

                290                                     300
Leu His Ser Asn Pro Asp Ser Pro Ala Lys Pro Gly Lys Asn Gly
CTA CAT AGC AAC CCT GAC AGT CCT GCC AAA CCA GAG AAG AAT GGG
                                                        900
                                      310
His Ala Lys Ile Val Asn Pro Arg Ile Ala Lys Phe Phe Glu Ile
CAC GCC AAG ATT GTC AAT CCC AGG ATT GCC AAG TTC TTT GAG ATC

                320                                     330
Gln Thr Met Pro Asn Gly Lys Thr Arg Thr Ser Leu Lys Thr Met
CAG ACC ATG CCC AAT GGC AAA ACC CGG ACC TCC CTT AAG ACG ATG
                                                        990
```

FIG. 1D

```
                                                     340
Ser Arg Arg Lys Leu Ser Gln Gln Lys Glu Lys Lys Ala Thr Gln
AGC CGC AGA AAG CTC TCC CAG CAG AAG GAG AAG AAA GCC ACT CAG

                 350                                    360
Met Leu Ala Ile Val Leu Gly Val Phe Ile Ile Cys Trp Leu Pro
ATG CTT GCC ATT GTT CTC GGT GTG TTC ATC ATC TGC TGG CTG CCC
                                                       1080
                                     370
Phe Phe Ile Thr His Ile Leu Asn Ile His Cys Asp Cys Asn Ile
TTC TTC ATC ACG CAC ATC CTG AAT ATA CAC TGT GAT TGC AAC ATC

                 380                                    390
Pro Pro Val Leu Tyr Ser Ala Phe Thr Trp Leu Gly Tyr Val Asn
CCA CCA GTC CTC TAC AGC GCC TTC ACA TGG CTG GGC TAT GTC AAC
                                                       1170
                                     400
Ser Ala Val Asn Pro Ile Ile Tyr Thr Thr Phe Asn Ile Glu Phe
AGT GCC GTC AAC CCC ATC ATC TAC ACC ACC TTC AAC ATC GAG TTC

                 410                 415
Arg Lys Ala Phe Met Lys Ile Leu His Cys
CGC AAG GCC TTC ATG AAG ATC TTG CAC TGC TGAGTCTGCCCCTTGCCTG
                                                       1264
```

FIG. 1E

CACAGCAGCTGCTTCCCACCTCCCTGCCTATGCAGGCCAGACCTCATCCCTGCAAGCTG

TGGGCAGAAAGGCCCAGATGAACTTGGCCTTCTCTCGACCCTGCAGGCCCTGCAGTGTTA
1383
GCTTGGCTCGATGCCCCTCTCTGCCCACACACCCTCATCCTGCCAGGGTAGGGCCAGGG

AGACTGGTATCTTACCAGCTCTGGGGTTGGACCCATGGCTCAGGGCAGCTCACAGAGTGC
1502
CCCTCTCATATCCAGACCCTGTCTCCTTGGCACCAAAGATGCAGCGGCCTTCCTTGACC

TTCCTCTTGGGCACAGAAACTAGCTCAGTGGTCGAGCACACCCTGATCGCTGGCTTGGCC
1621
TGGCCCTTGCTTGCCTGTGCCGGATCAGGTGGTGGGAGGGAGCGACACGTTCTTACTTT

ATAGGAACCACATAGGAAAGCAGGGAACACGCCAAGTCCTCCAGGCACATCAGTGTCAGG
1740
AGACACACATAAACACCAGGTAGCTCCATGGACCCCAGAGAAACTGAGGCTGAAAAATC

TGTTTTCCACTCCAACTCTAGTGTGAGTCCCTACTTTTCATAGCCATGGGTATTACTATG
1859

FIG. 1F

TCCTACCTTGTTATAGTATCCCATGGGGTTTCTGTACCATTTGGGGAAAACAACTCTA

ATCCTCAAGGGCCCCAAGAGAATCTGTAAGGAGAAAAATAGGCTGATCTCCCTCTACTCT 1978

CCAATCCACTCCACCACTTCTTGATATACCTTGGATGTATCCATTCCTCACAGCAAATG

CTGGCCAGTCAGGCCTTGGACCAGTGTTGGAGTTGAAGCTGGATGTGGTAACTTGGGGCT 2097

CTTTGGGGCTGGGGGGGTTGTTAACATCGTCTCTCTTCCATATCTCTTCCTTCCCAGTG

CCTCTGCCTTAGAAGAGGCTGTGGATGGGGTGCTGGGACTGCTGATACCATTGGGCCTGG 2216

CCCTGAATGAGGAGGGGAAGCTGCAGTTTGGAGGGTTCTGGGATCCAACTCTGTAACAT

CACTATACCTGTACCAAAACTAATAAAACCTTGACAAGAGTCAAAAAAAAAAA 2317

FIG. 1G

```
                                                                  I
Dδ    MD....PL...NISWYDDDLERQNWSRPFNGSEGKADRPHYNYYAMIITLL.IFIIVFGNVLVCMAVSREKALQTITNY
βδ    MGP...P...GNDSDFLLTTNGSHV...PDHDVTEERDEAWVVGMAIIMSVIVLAIVFGNVLVITAIAKFERLQTVTNY
αδ    MGSLQ.PQA.GNASWNGTEAPG..GGARATPYSLQVT....LTLVCLAGLL.MLLTVFGNVLVIIAVFTSRAIKAPQNL
G-21  MDVLS.PGQ.QNNTTSPPAPFE..TGGNTTGISDVTVSYQV.ITSLIIGTLL.IFCAVIGNACVVAAIALERSLQNVANY
M1    MNTSAPPAVSPNITVLAP.....GKGPWQVA..........FIGITTGLL.SLATVTGNILVIISFKVNTELKTVNNY
SK    MGACV.VMTDINIS.......SGLDSNATGITAFSMPGWQLALWTAAYLAL.VLVAVMGNATVIWIILAHQRMRIVTNY

           II                                  III
Dδ    LIVSLAMADIIVATLVMPWVVYLEVVGEWKFSRIHCDIFVTLDVMMCTASILNLCAISIQRYTAVAMPMIYMTRYSSKRR
βδ    FIDSLACADLVMGIAVVPFGASHIIMKMWNFGNFWCEFWTSIQVLCVTASIETLCVIAVQRYIAITSPFKYQSLLTKNKA
αδ    FIVSLASADILVATLVIPFSLANEVMQYWYFGKTWCEIYLALDVLFCTSSIVHLCAISIQRYWSITQAIEYNLKRTPRRI
G-21  LIGSLAVTDIMVSVLVIPMAALYQVLNNWTLGQVTCDLFIALDVLQCTSSILHLCAIAIQRYWAITDPIDYVNKRTPRPR
M1    FLLSLACADLIIGIFSMNLYTTYLLMQIWALGTLACDLWLALDYVASNASVMNLLIISFQRYFSVTRPLSYRAKTRPRRA
SK    FIVNLALADICMAAFNAAFNFVYASHNIWYFGRAFCYFQNLFPITAMFVSIYSMTAIAAQRYMAIVRPFQPRLSAPGTR.

           IV                                                      V
Dδ    VTVMIAIVWVISFTISC.PLLFGLNNTD.........QNECIIANPAFVVYSSIMSFYVPFIVTLLVYIKIYIVLRKRRKRVNTKR-(111)
βδ    RMV.ILMVWIVSGLTSFIPIQMHWYRATH..QKAIDCYHRETCCDFFTNQAYAIWSSIVSFYVPLIVMVFVYSRVFQVAKRQLQKI-(32)-
αδ    KAI.IITVWVISAVISFPPLISIEKKGGG.....GGPQPAEPRCEINDQKWYVISSCIGSFFAPQLIMILVYVRIYQIAKRRTRVP-(137)
G-21  ALT.SLT.WLIGFLLSIPPMLGWRTPEDR.........SDPDACTISKDMGYTIYSTFGAFYIPLLLMLVLYGRIFRAARFRIPKT-(110)
M1    ALM.IGLAWLVSFVLWA.PAILFWQYLVGE....RTVLAGQCYIQFLSQPIITFGTAMAAFYLPVTVMCTIYWRIYRETENRAREL-(137)
SK    .AV.IAGIWLVALALAF.PQCFYSTITTDEGATKCVVAWPEDSGGKMLLLYHLIVIALIYF.LPLVVMFVAYSVIGLTLWRRSVPG-(12)-

             VI                                             VII
Dδ    -KEKKATQMIAIVIGMFIICWLPFFITHIINIHCQCN....IPPVLYSAFTWLGYVNSA..VNPIIYTTFNIEFRNAFMKILHC
βδ    -KEHKALKTLGIIMGIFTLCWLPFFIVNIVHVIQDNL....IPKEVYILLNWLGYVNSA..PNPIIYCRSP.DFRIAFQEIL.CL--(36)
αδ    -REKRFTFVLAVVIGMFVVCWFPFFFTYTLTAVGCS.....VPRTLFKFFFWFGYCNSS..LNPVIYTLFNHDFRRAFWKIL.CRC--(6)
G-21  -RERKTVKTLQIIMGIFILCWLPFFIVALVLPPCESSC..HMPTILGAIINWLGYSNSL..INPVIYAYFNKDFQNAFWKIIKCNFCRQ
M1    -KEKKAARTLSAILLAFIVTWIYNIMVLVSTFCKDC.....VPETLWELGYWICYVNST..LNPMCYALCNKAFRDTFRLLLHCR--(24)
SK    -AKKKFVKTMVIVVVTFAICWLPYHLYFIIGTFQEDIYCHKFIQQVYLALPWIA..MSSTMYNPIIYCCINHRFRSQFRLAPRCC--(62)
```

FIG. 2

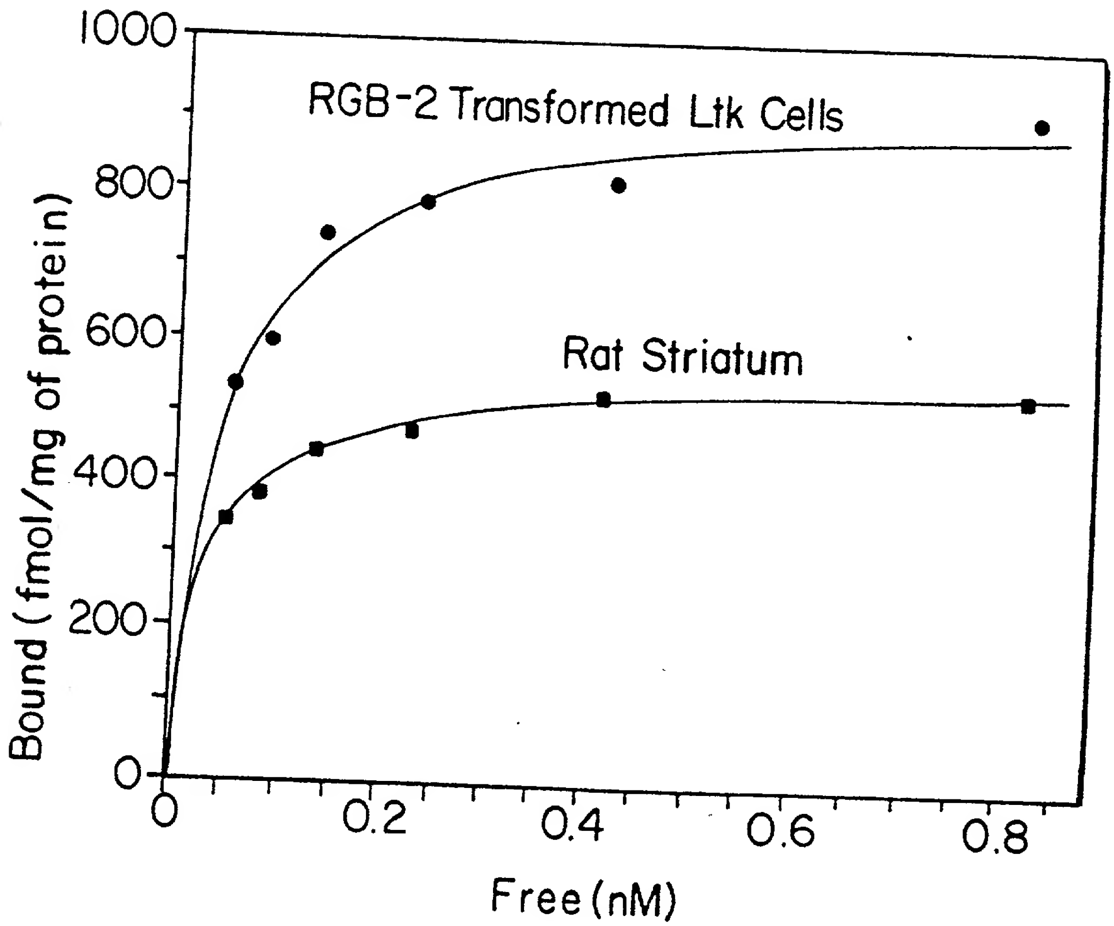


FIG. 4A-1

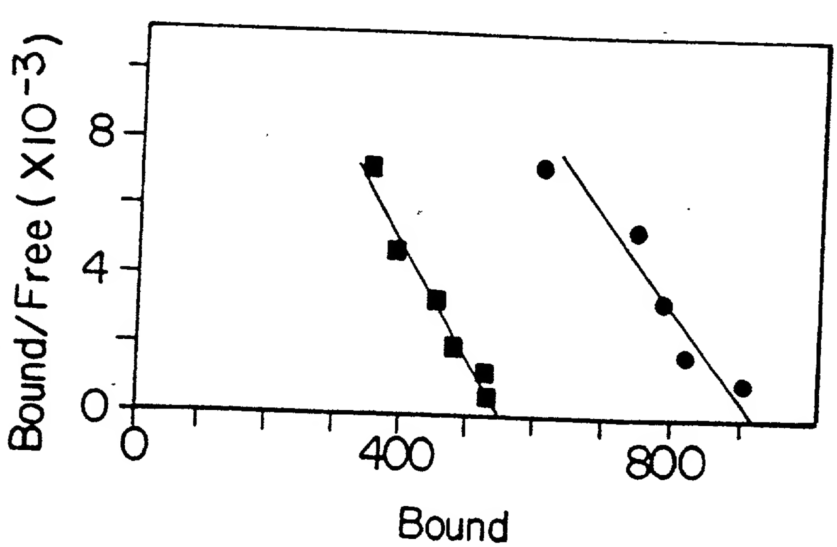
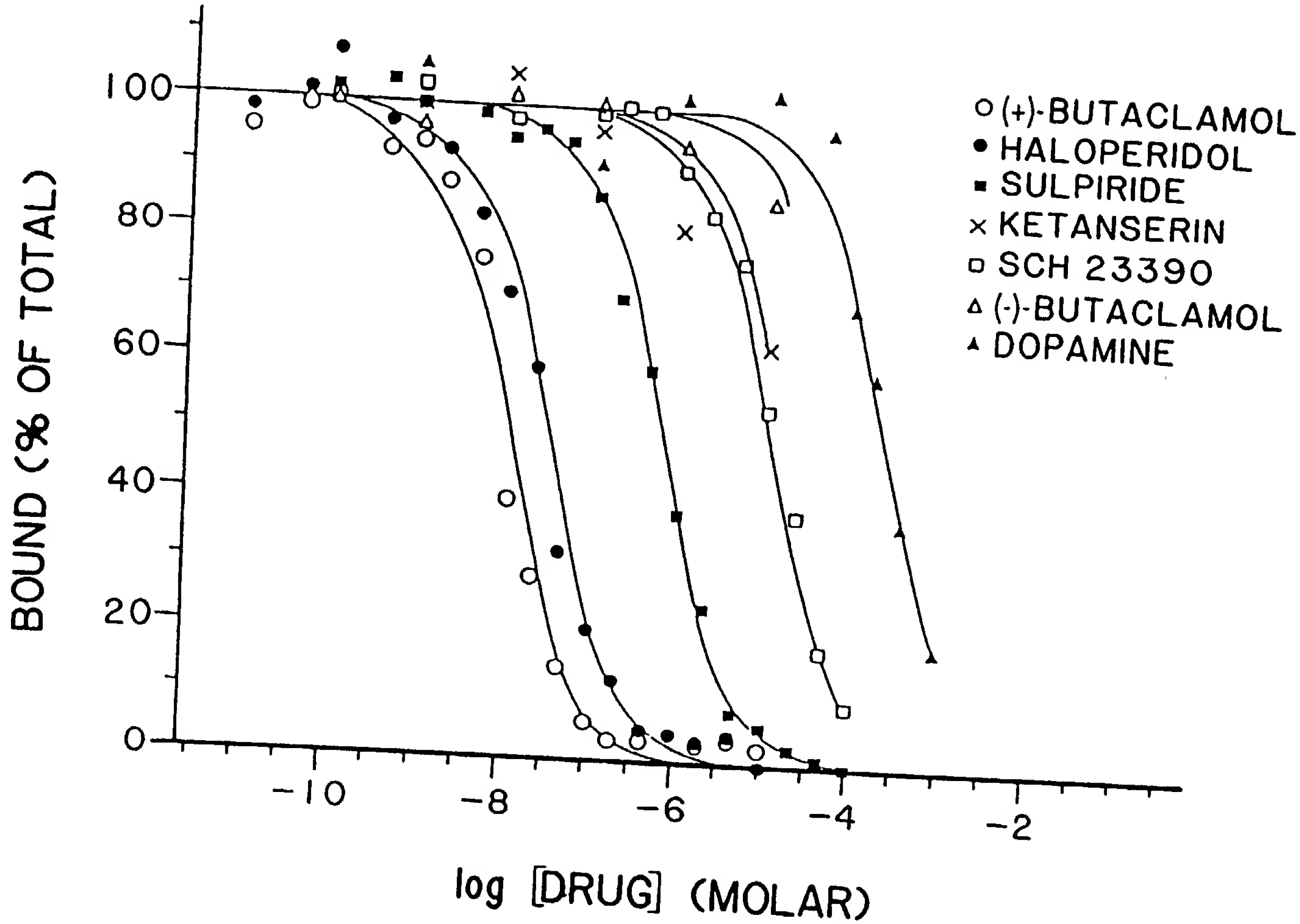


FIG. 4A-2

SCANNED,# 10

FIG. 4B



TOT280"8SEhE660

DRUG	Ki (nM)	
	RGB-2	
	Transformed Ltk-Cells	Rat Striatum
(+)-Butaclamol	0.83	1.0
(-)-Butaclamol	>1,000	>1,000
Haloperidol	3.0	5.3
Dopamine + GTP	17,000	6,300
Sulpiride		
high affinity	80	67 (87%)
low affinity	---	>10,000 (13%)
SCH 23390		
high affinity	---	35 (16%)
low affinity	1,000	780 (84%)
Ketanserin		
high affinity	---	27 (25%)
low affinity	>1,000	>1,000 (75%)

FIG. 4C

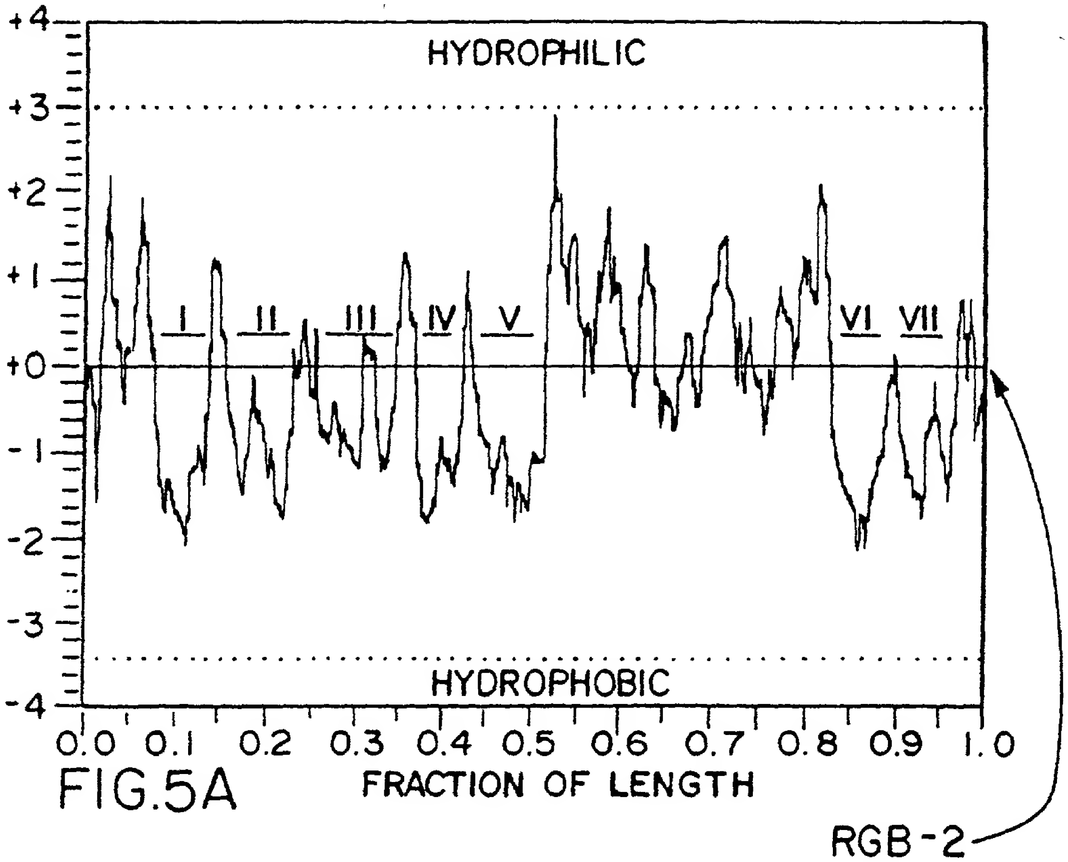

HYDROPHILIC
HYDROPHOBIC
I
II
III
IV
V
VI
VII
+4
+3
+2
+1
+0
-1
-2
-3
-4
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
FRACTION OF LENGTH
RGB-2

FIG.5A

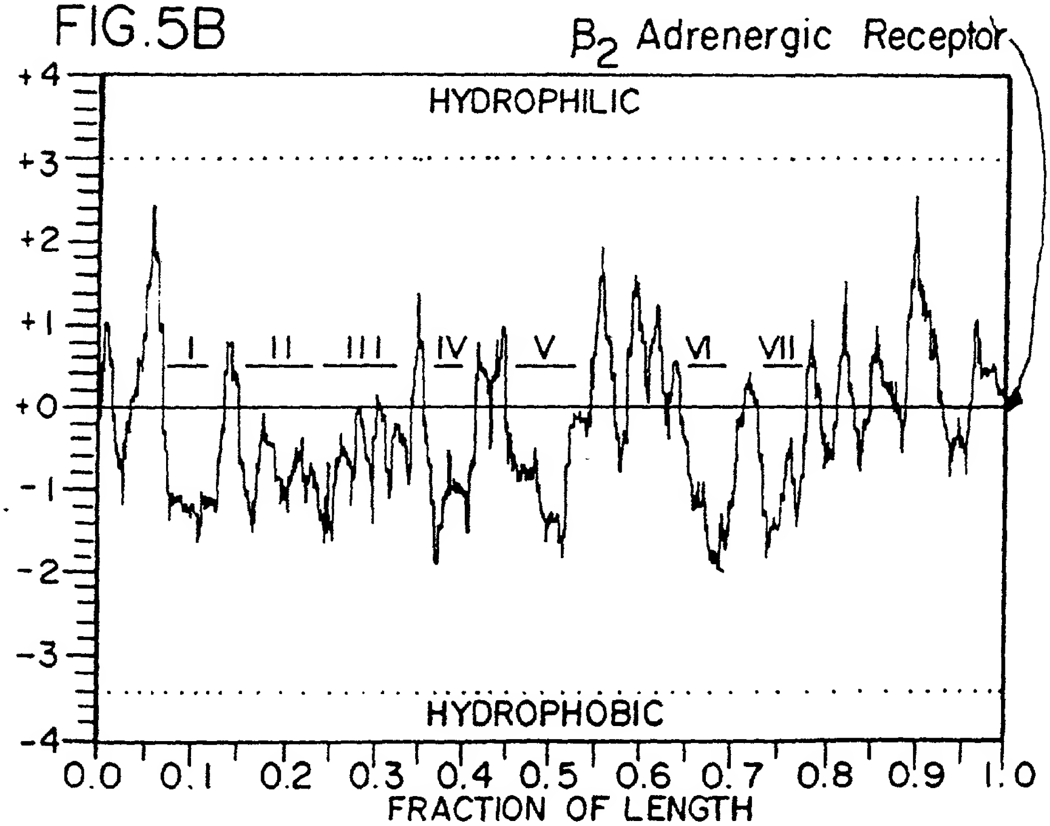
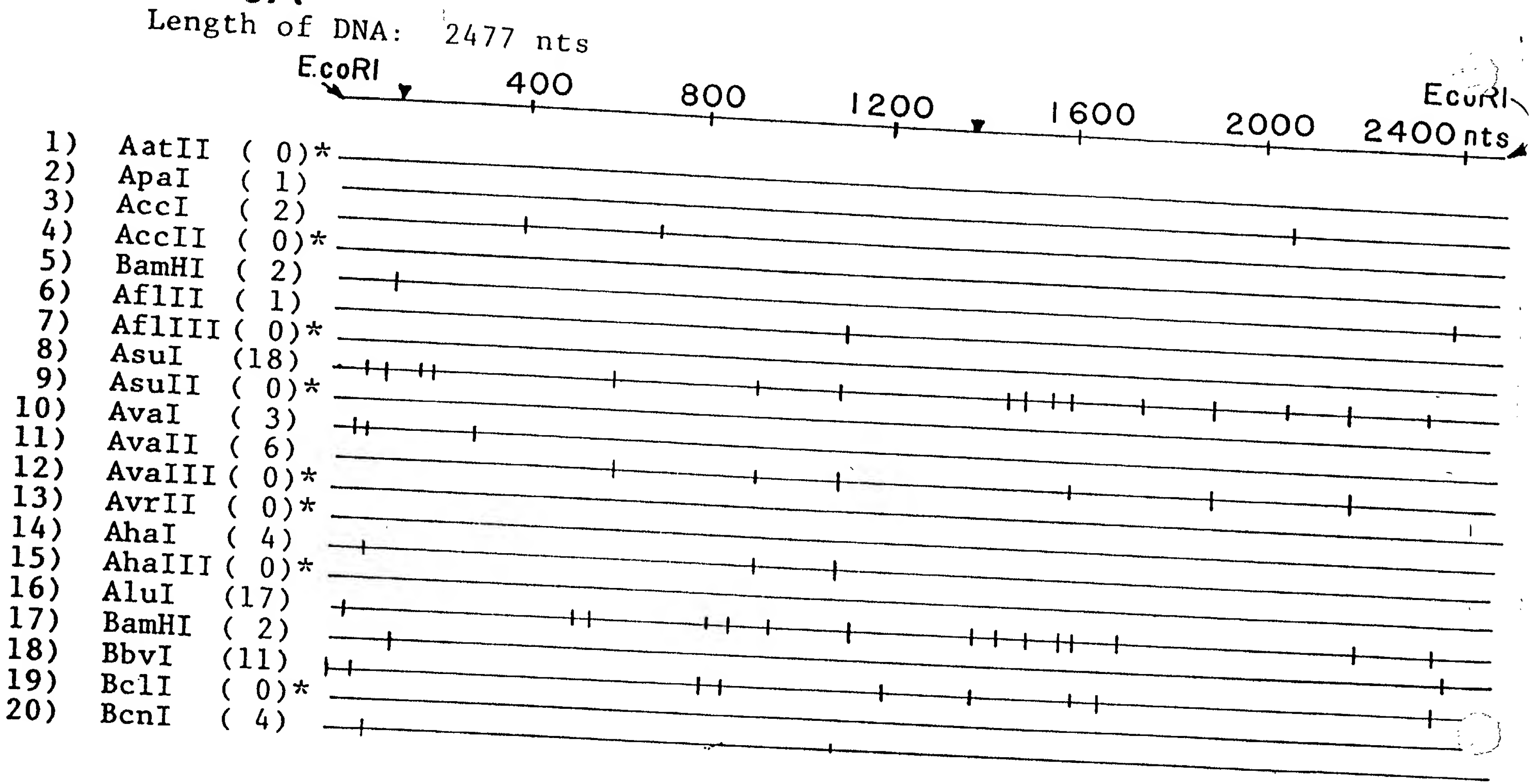

β_2 Adrenergic Receptor
HYDROPHILIC
HYDROPHOBIC
I
II
III
IV
V
VI
VII
+4
+3
+2
+1
+0
-1
-2
-3
-4
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
FRACTION OF LENGTH

FIG.5B

FIG. 6A


Length of DNA: 2477 nts
EcoRI
400
800
1200
1600
2000
2400 nts
EcoRI
1) AatII (0)*
2) ApaI (1)
3) AccI (2)
4) AccII (0)*
5) BamHI (2)
6) AflII (1)
7) AflIII (0)*
8) AsuI (18)
9) AsuII (0)*
10) AvaI (3)
11) AvaII (6)
12) AvaIII (0)*
13) AvrII (0)*
14) AhaI (4)
15) AhaIII (0)*
16) AluI (17)
17) BamHI (2)
18) BbvI (11)
19) BclI (0)*
20) BcnI (4)

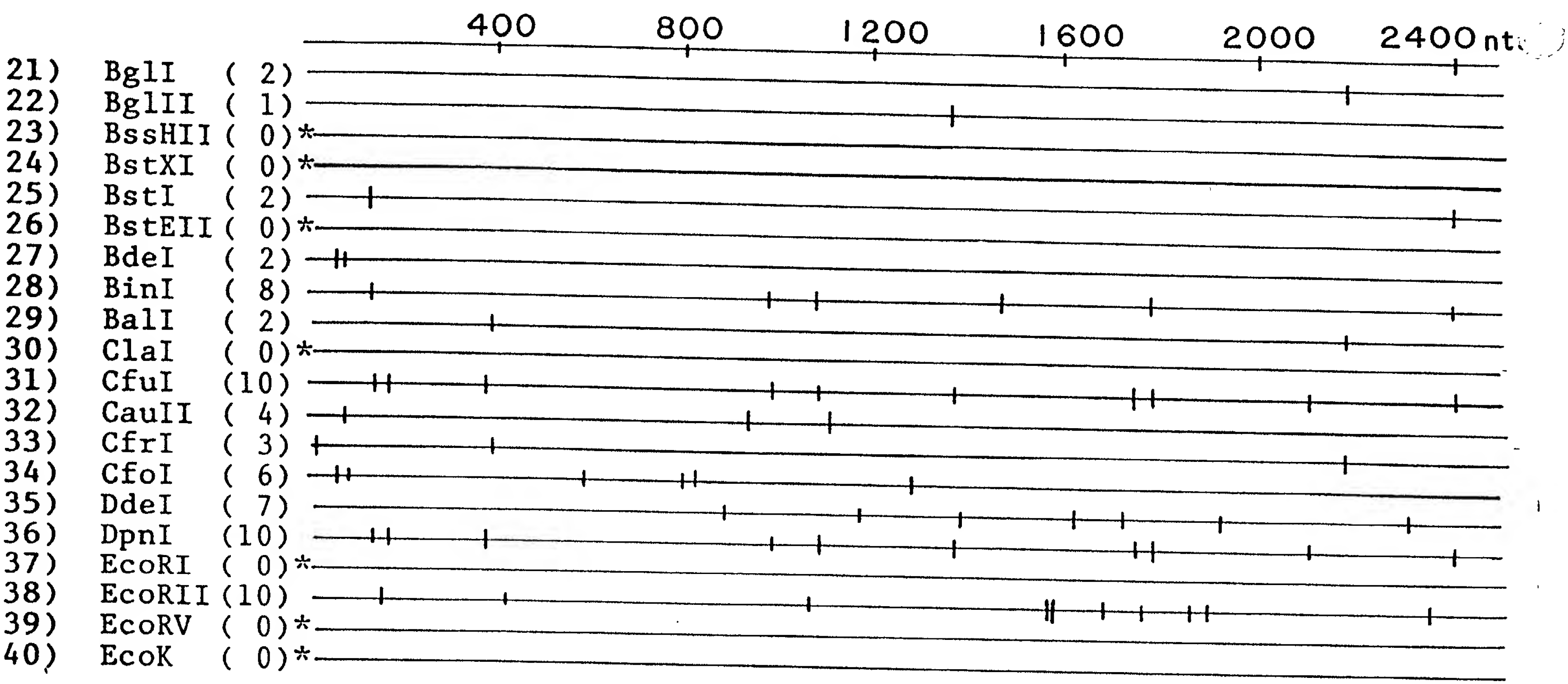

400
800
1200
1600
2000
2400 nt
21) BglI (2)
22) BglII (1)
23) BssHII (0)*
24) BstXI (0)*
25) BstI (2)
26) BstEII (0)*
27) BdeI (2)
28) BinI (8)
29) BalI (2)
30) ClaI (0)*
31) CfuI (10)
32) CauII (4)
33) CfrI (3)
34) CfoI (6)
35) DdeI (7)
36) DpnI (10)
37) EcoRI (0)*
38) EcoRII (10)
39) EcoRV (0)*
40) EcoK (0)*

FIG. 6B

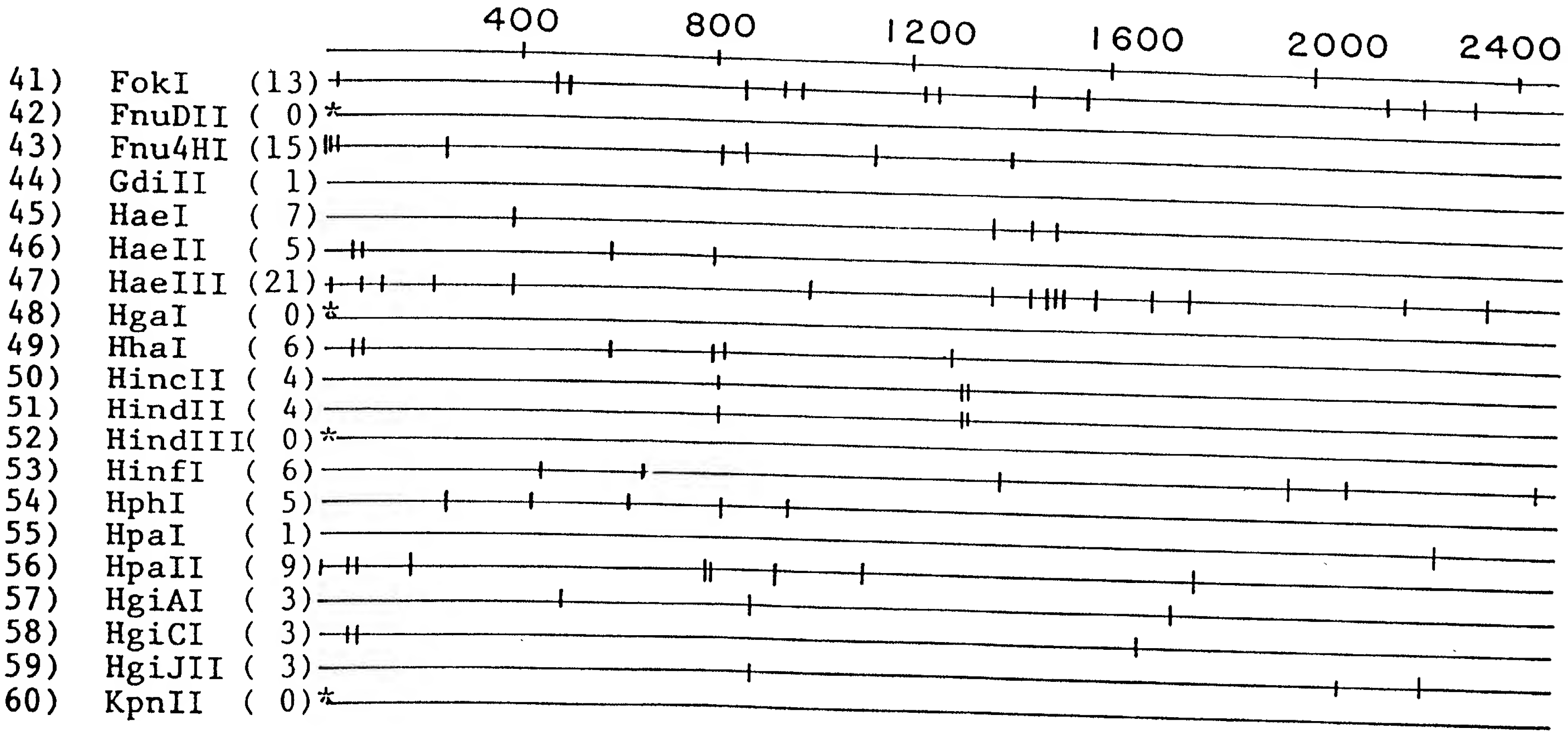

400
800
1200
1600
2000
2400 nts
41) FokI (13)
42) FnuDII (0)*
43) Fnu4HI (15)
44) GdiII (1)
45) HaeI (7)
46) HaeII (5)
47) HaeIII (21)
48) HgaI (0)*
49) HhaI (6)
50) HincII (4)
51) HindII (4)
52) HindIII(0)*
53) HinfI (6)
54) HphI (5)
55) HpaI (1)
56) HpaII (9)
57) HgiAI (3)
58) HgiCI (3)
59) HgiJII (3)
60) KpnII (0)*

FIG. 6C

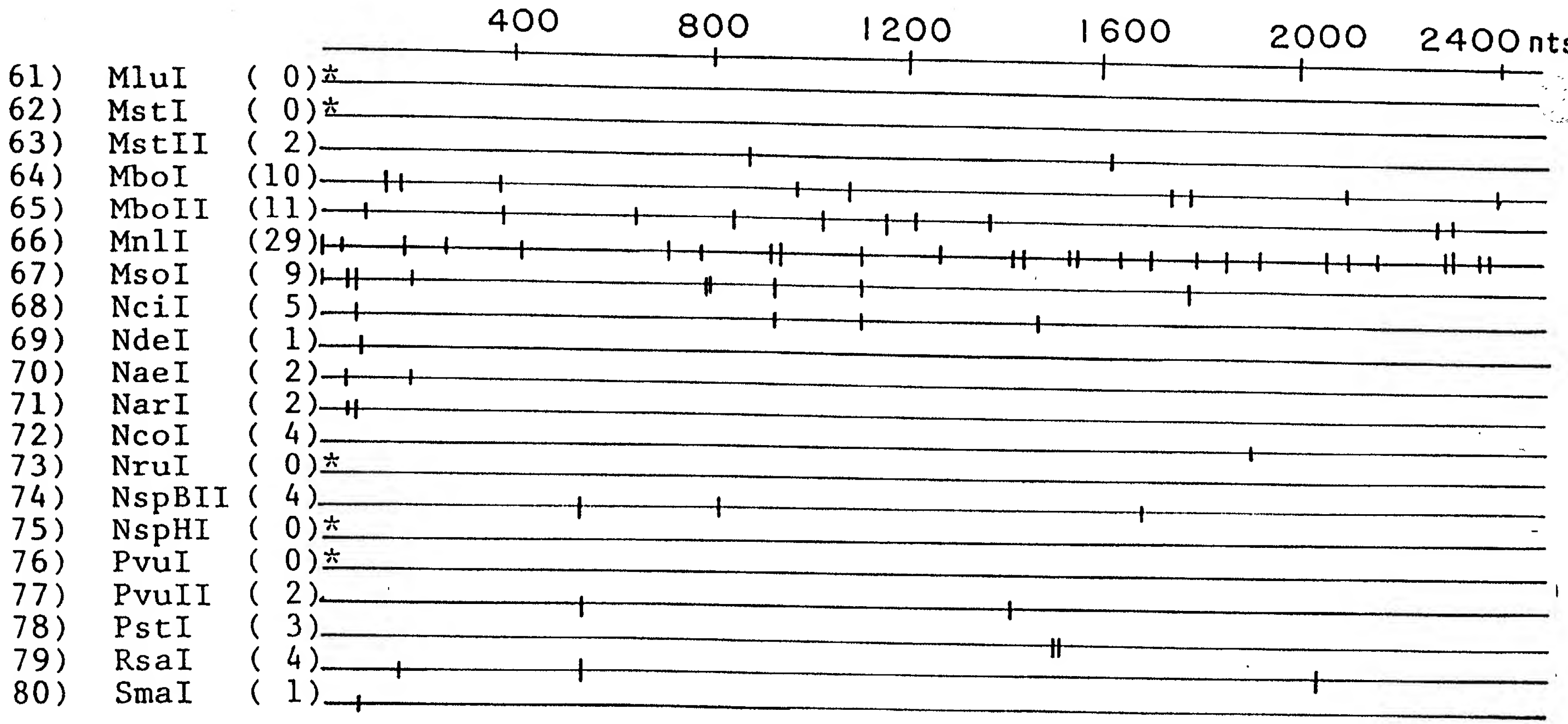

400
800
1200
1600
2000
2400 nts
61) MluI (0)*
62) MstI (0)*
63) MstII (2)
64) MboI (10)
65) MboII (11)
66) MnlI (29)
67) MsoI (9)
68) NciI (5)
69) NdeI (1)
70) NaeI (2)
71) NarI (2)
72) NcoI (4)
73) NruI (0)*
74) NspBII (4)
75) NspHI (0)*
76) PvuI (0)*
77) PvuII (2)
78) PstI (3)
79) RsaI (4)
80) SmaI (1)

FIG. 6D

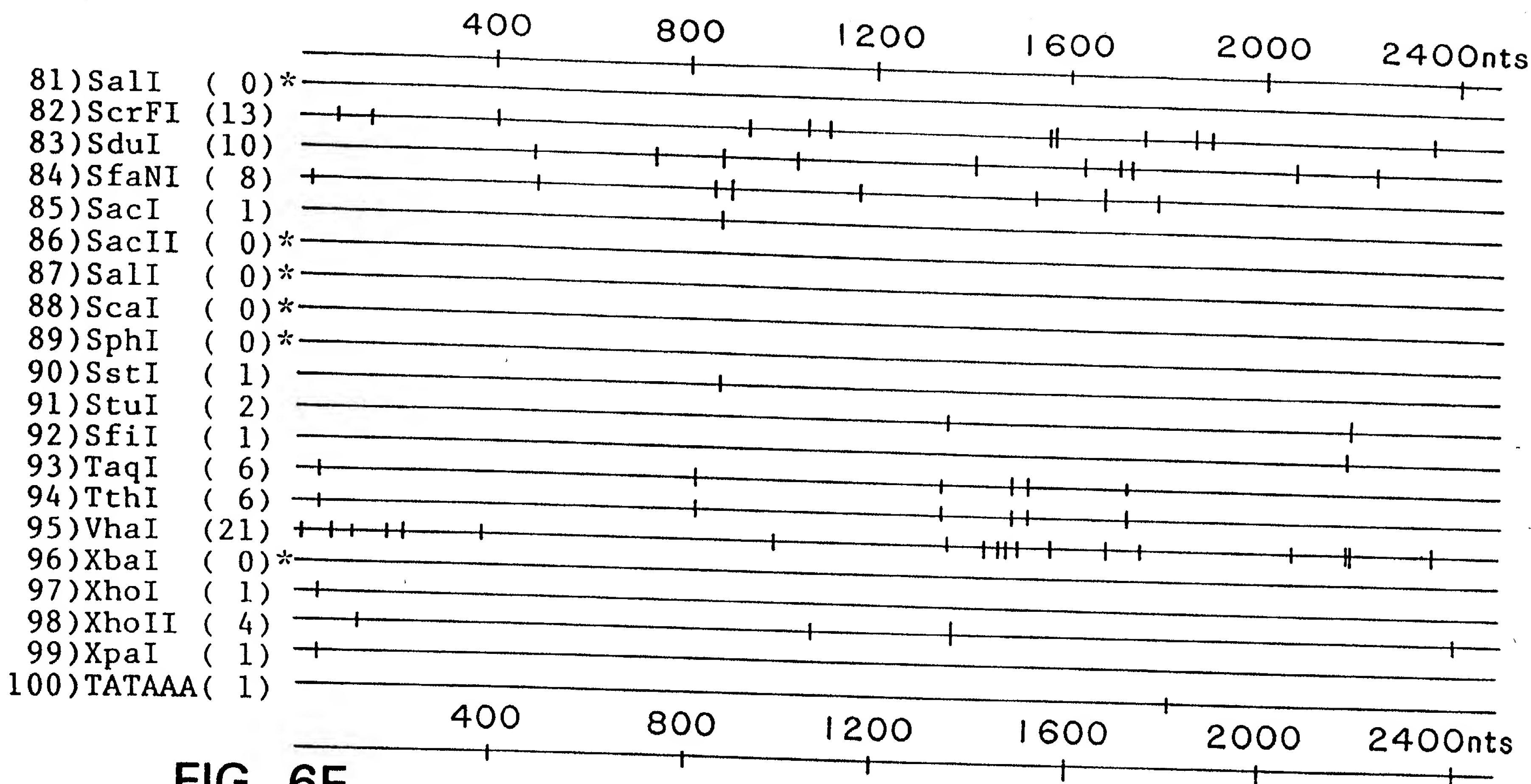

400
800
1200
1600
2000
2400nts
81)SalI (0)*
82)ScrFI (13)
83)SduI (10)
84)SfaNI (8)
85)SacI (1)
86)SacII (0)*
87)SalI (0)*
88)ScaI (0)*
89)SphI (0)*
90)SstI (1)
91)StuI (2)
92)SfiI (1)
93)TaqI (6)
94)TthI (6)
95)VhaI (21)
96)XbaI (0)*
97)XhoI (1)
98)XhoII (4)
99)XpaI (1)
100)TATAAA(1)
400
800
1200
1600
2000
2400nts

FIG. 6E

FIG. 7A

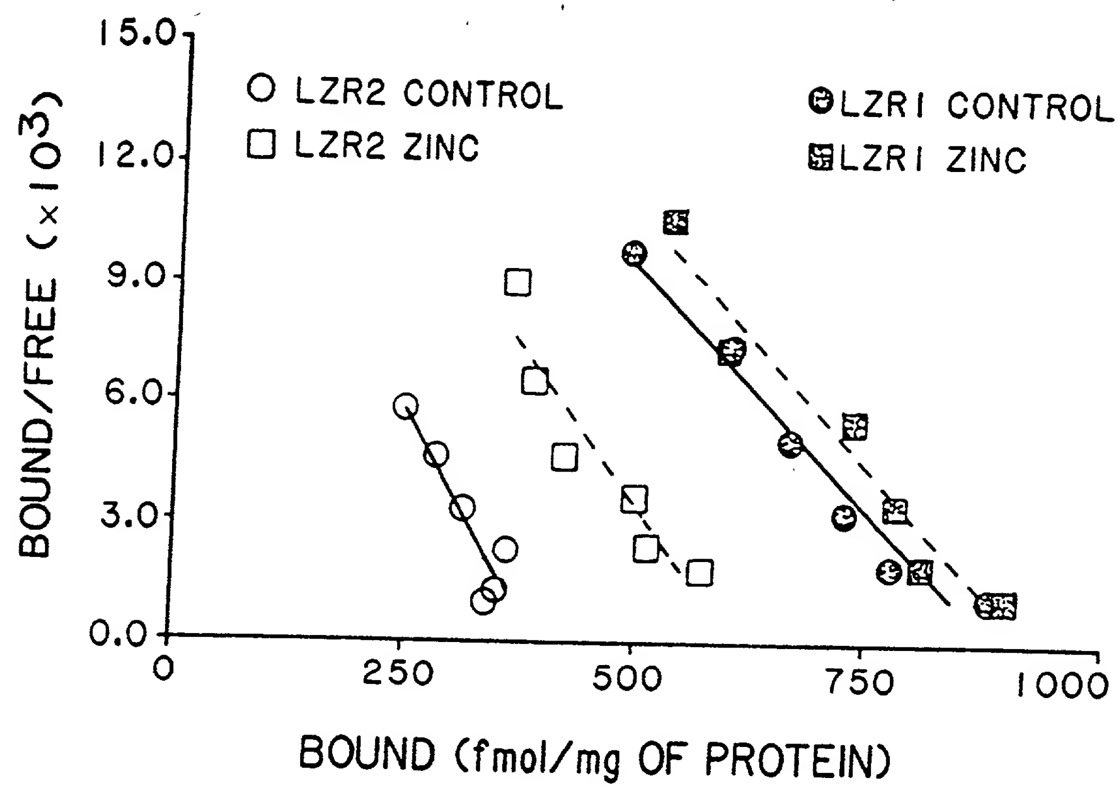
```
                                           27                                                   54
3'GTC GGG TGG GCT CTC CTG GGC CAT GTC GGG GTA GGG TGG GTC GGT GGT GGT CGA 5'
5'CAG CCC ACC CGA GAG GAC CCG GTA CAG CCC CAT CCC ACC CAG CCA CCA CCA GCT 3
  Gln Pro Thr Arg Glu Asp Pro Val Gln Pro His Pro Thr Gln Pro Pro Pro Ala
   Ser Pro Pro Glu Arg Thr Arg Tyr Ser Pro Ile Pro Pro Ser His His Gln Leu
    Ala His Pro Arg Gly Pro Gly Thr Ala Pro Ser His Pro Ala Thr Thr Ser

                                           81                                                  108
  CTG AGA GGG GCT GGG CAG GGT GGT ACC AGA GGT GTC GTG AGG GCT GTC GGG GCG
  GAC TCT CCC CGA CCC GTC CCA CCA TGG TCT CCA CAG CAC TCC CGA CAG CCC CGC
  Asp Ser Pro Arg Pro Val Pro Pro Trp Ser Pro Gln His Ser Arg Gln Pro Arg
   Thr Leu Pro Asp Pro Ser His His Gly Leu His Ser Thr Pro Asp Ser Pro Ala
    Leu Ser Pro Thr Arg Pro Thr MET Val Ser Thr Ala Leu Pro Thr Ala Pro Pro

                                          135                                                  162
  GTT TGG TCT CTT CTT ACC CGT ACG GTT TTC CTG GTG GGG TTC CTA ACG GTT CTA
  CAA ACC AGA GAA GAA TGG GCA TGC CAA AAG GAC CAC CCC AAG GAT TGC CAA GAT
  Gln Thr Arg Glu Glu Trp Ala Cys Gln Lys Asp His Pro Lys Asp Cys Gln Asp
   Lys Pro Glu Lys Asn Gly His Ala Lys Arg Thr Thr Pro Arg Ile Ala Lys Ile
    Asn Gln Arg Arg MET Gly MET Pro Lys Gly Pro Pro Gln Gly Leu Pro Arg Ser

                                          189                                                  216
  GAA ACT CTA GGT CTG GTA CGG GTT ACC GTT TTG GGC CTG GAG GGA GTT CTG GTA
  CTT TGA GAT CCA GAC CAT GCC CAA TGG CAA AAC CCG GAC CTC CCT CAA GAC CAT
  Leu  .  Asp Pro Asp His Ala Gln Trp Gln Asn Pro Asp Leu Pro Gln Asp His
   Phe Glu Ile Gln Thr MET Pro Asn Gly Lys Thr Arg Thr Ser Leu Lys Thr MET
```

FIG. 7B

```
                                        243                                               270
CTC GGC ATC CTT C6A G55 GGT CGT CTT CCT CTT CTT TCG GTG AGT CTA CGA GCG
GAG CCG TAG GAA G3T C44 CCA GCA GAA GGA GAA GAA AGC CAC TCA GAT GCT CGC
Glu Pro  .  Glu C    TT Pro Ala Glu Gly Glu Glu Ser His Ser Asp Ala Arg
 Ser Arg Arg Lys Leu Phe Gln Gln Lys Glu Lys Lys Ala Thr Gln MET Leu Ala
  Ala Val Gly     Ser     Ser Arg Arg Arg Arg Lys Pro Leu Arg Cys Ser Pro

                                        297                                               324
GTA 5CA AGA GCC GCA CAA GTA GTA GAC GAC CGA CGG GAA GAA GTA GTG TGT GTA
CAT 4GT TCT CGG CGT GTT CAT CAT CTG CTG GCT GCC CTT CTT CAT CAC ACA CAT
His T   Ser Arg Arg Val His His Leu Leu Ala Ala Leu Leu His His Thr His
 ILE Val Leu Gly Val Phe Ile Ile Cys Trp Leu Pro Phe Phe Ile Thr His Ile
  le  Phe Ser Ala Cys Ser Ser Ser Ala Gly Cys Pro Ser Ser Ser His Thr Ser

                                        351                                               378
GGA CTT GTA TGT GAC ACT GAC GTT GTA GGG CGG ACA GGA CAT GTC GCG GAA GTG
CCT GAA CAT ACA CTG TGA CTG CAA CAT CCC GCC TGT CCT GTA CAG CGC CTT CAC
Pro Glu His Thr Leu  .  Leu Gln His Pro Ala Cys Pro Val Gln Arg Leu His
 Leu Asn Ile His Cys Asp Cys Asn Ile Pro Pro Val Leu Tyr Ser Ala Phe Thr
  .  Thr Tyr Thr Val Thr Ala Thr Ser Arg Leu Ser Cys Thr Ala Pro Ser Arg

                                        405                                               432
CAC CGA CCC GAT ACA GTT GTC GCG GCA CTT GGG GTA GTA GAT GTG GTG GAA GTT
GTG GCT GGG CTA TGT CAA CAG CGC CGT GAA CCC CAT CAT CTA CAC CAC CTT CAA
Val Ala Gly Leu Cys Gln Gln Arg Arg Glu Pro His His Leu His His Leu Gln
 Trp Leu Gly Tyr Val Asn Ser Ala Val Asn Pro Ile Ile Tyr Thr Thr Phe Asn
  Gly Trp Ala MET Ser Thr Ala Pro  .  Thr Pro Ser Ser Thr Pro Pro Ser Thr
```

```
                                        459                                        486
GTA ACT CAA GGC GTT CCG GAA GGA CTT CTA GGA GGT GAC GAC TGA GAC GAC GGA
CAT TGA GTT CCG CAA GGC CTT CCT GAA GAT CCT CCA CTG CTG ACT CTG CTG CCT
His  .  Val Pro Gln Gly Leu Pro Glu Asp Pro Pro Leu Leu Thr Leu Leu Pro
 Ile Glu Phe Arg Lys Ala Phe Leu Lys Ile Leu His Cys STOPLeu Cys Cys Leu
  Leu Ser Ser Ala Arg Pro Ser  .  Arg Ser Ser Thr Ala Asp Ser Ala Ala Cys

                                        513                                        540
CGG CGT GTC GTC GGA CGA AGG GTG GAG GGA CGG GTC ACG GCC GGT CGG AGT GGG
GCC GCA CAG CAG CCT GCT TCC CAC CTC CCT GCC CAG TGC CGG CCA GCC TCA CCC
Ala Ala Gln Gln Pro Ala Ser His Leu Pro Ala Gln Cys Arg Pro Ala Ser Pro
 Pro His Ser Ser Leu Leu Pro Thr Ser Leu Pro Ser Ala Gly Gln Pro His Pro
  Arg Thr Ala Ala Cys Phe Pro Pro Pro Cys Pro Val Pro Ala Ser Leu Thr Leu

                                        567                                        594
AAC GCT TGG CAC TCG TCC TTC CGG ACC CAC CTA GCC GGA GGA GAA GAT CGG GGC
TTG CGA ACC GTG AGC AGG AAG GCC TGG GTG GAT CGG CCT CCT CTT CTA GCC CCG
Leu Arg Thr Val Ser Arg Lys Ala Trp Val Asp Arg Pro Pro Leu Leu Ala Pro
 Cys Glu Pro  .  Ala Gly Arg Pro Gly Trp Ile Gly Leu Leu Phe  .  Pro Arg
  Ala Asn Arg Glu Gln Glu Gly Leu Gly Gly Ser Ala Ser Ser Ser Ser Pro Gly
```

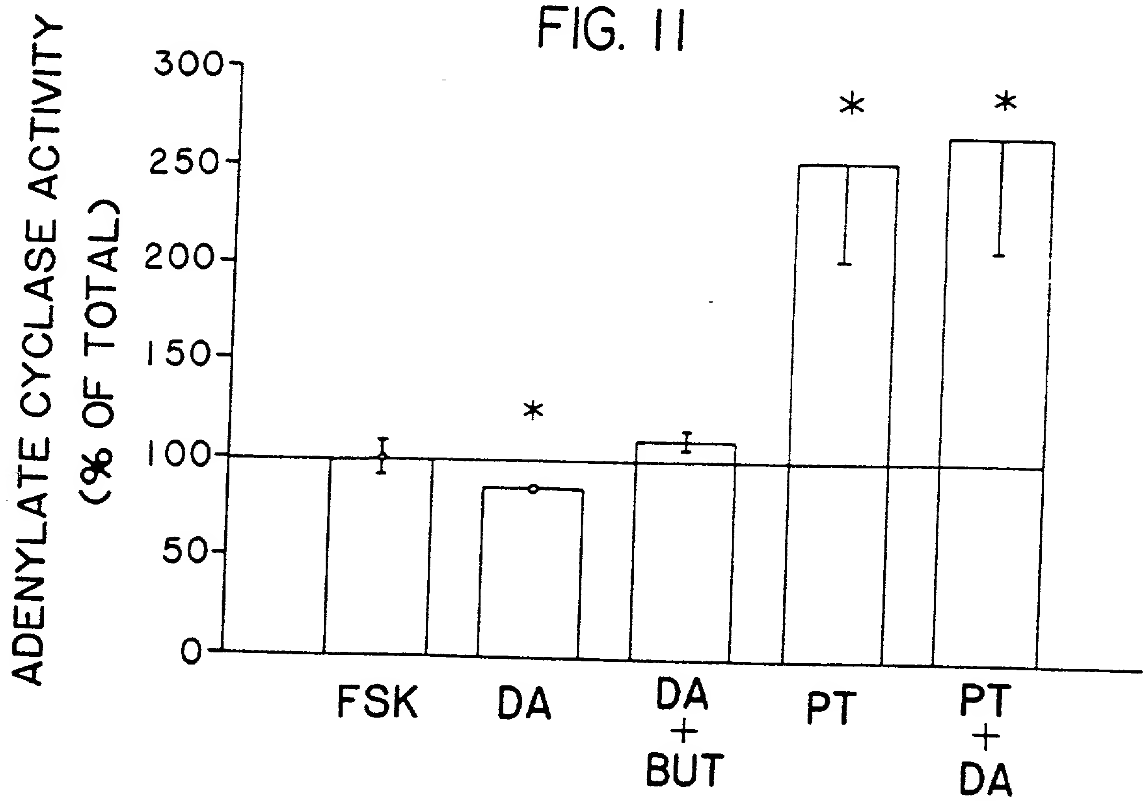
FIG. 7C



15.0
12.0
9.0
6.0
3.0
0.0
BOUND/FREE (x 10^3)
LZR2 CONTROL
LZR2 ZINC
LZR1 CONTROL
LZR1 ZINC
0
250
500
750
1000
BOUND (fmol/mg OF PROTEIN)

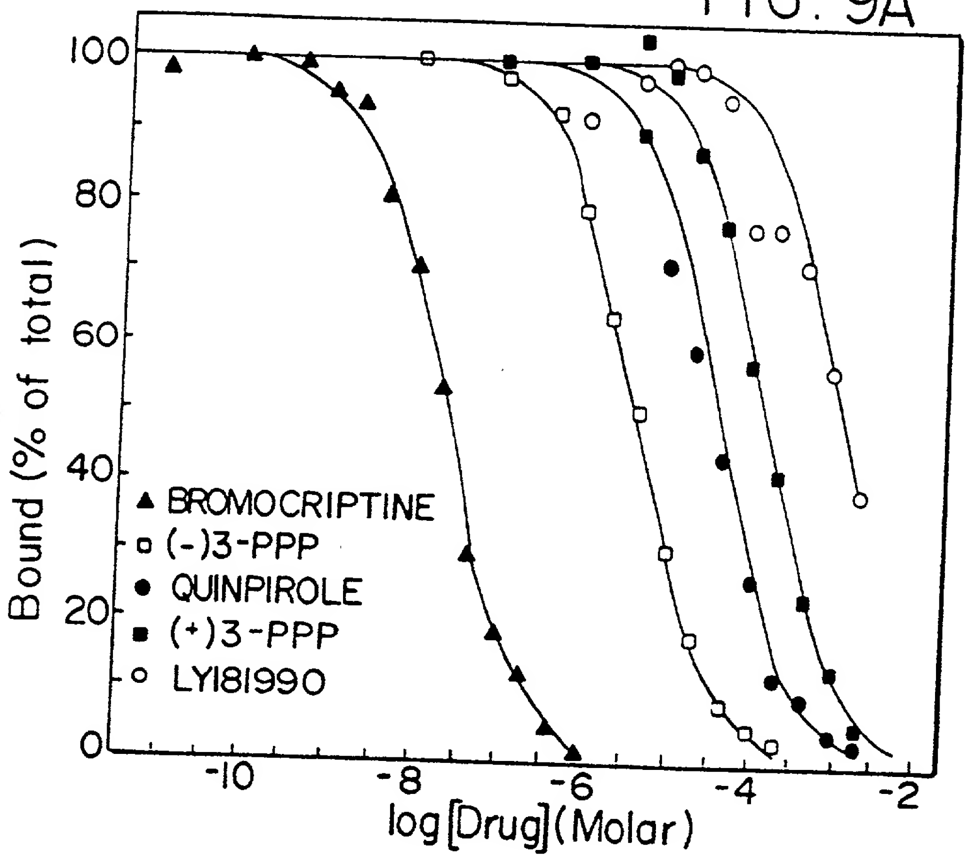
FIG. 8

FIG. 11



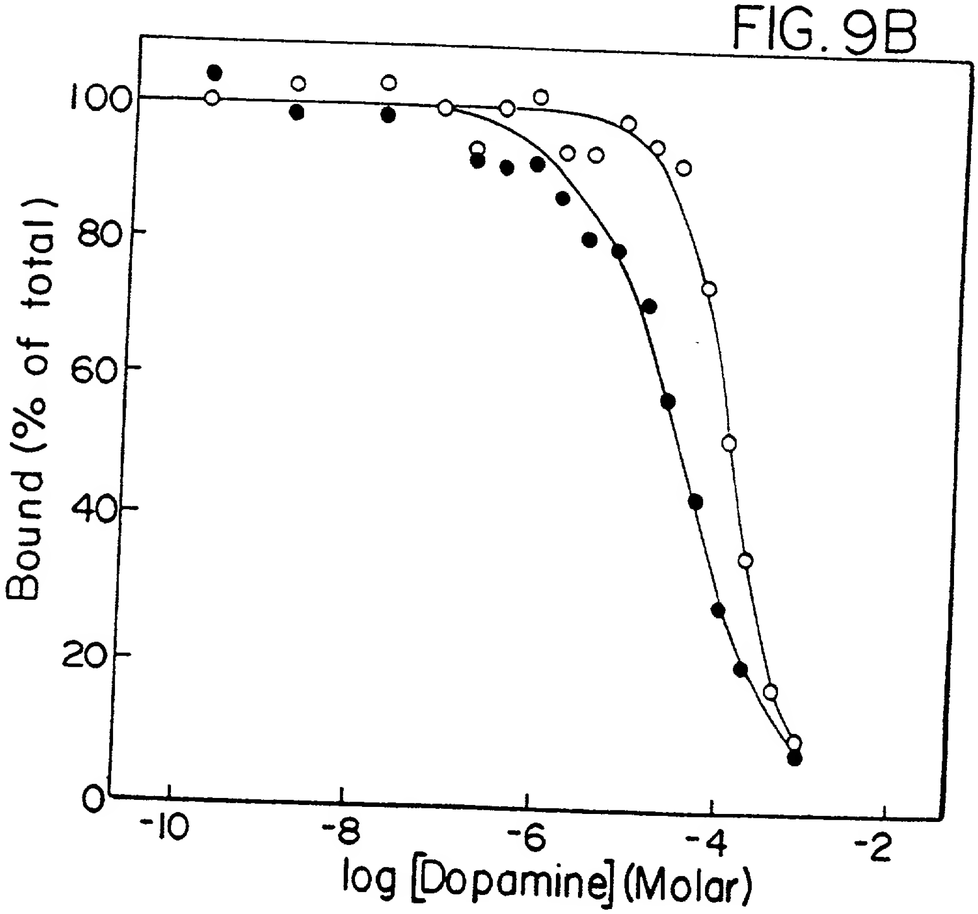
ADENYLATE CYCLASE ACTIVITY (% OF TOTAL)
300
250
200
150
100
50
0
*
*
*
FSK
DA
DA + BUT
PT
PT + DA

FIG. 9A



100
80
60
40
20
0
Bound (% of total)
BROMOCRIPTINE
(-)3-PPP
QUINPIROLE
(+)3-PPP
LY181990
-10
-8
-6
-4
-2
log [Drug] (Molar)

FIG. 9B



100
80
60
40
20
0
Bound (% of total)
-10
-8
-6
-4
-2
log [Dopamine] (Molar)

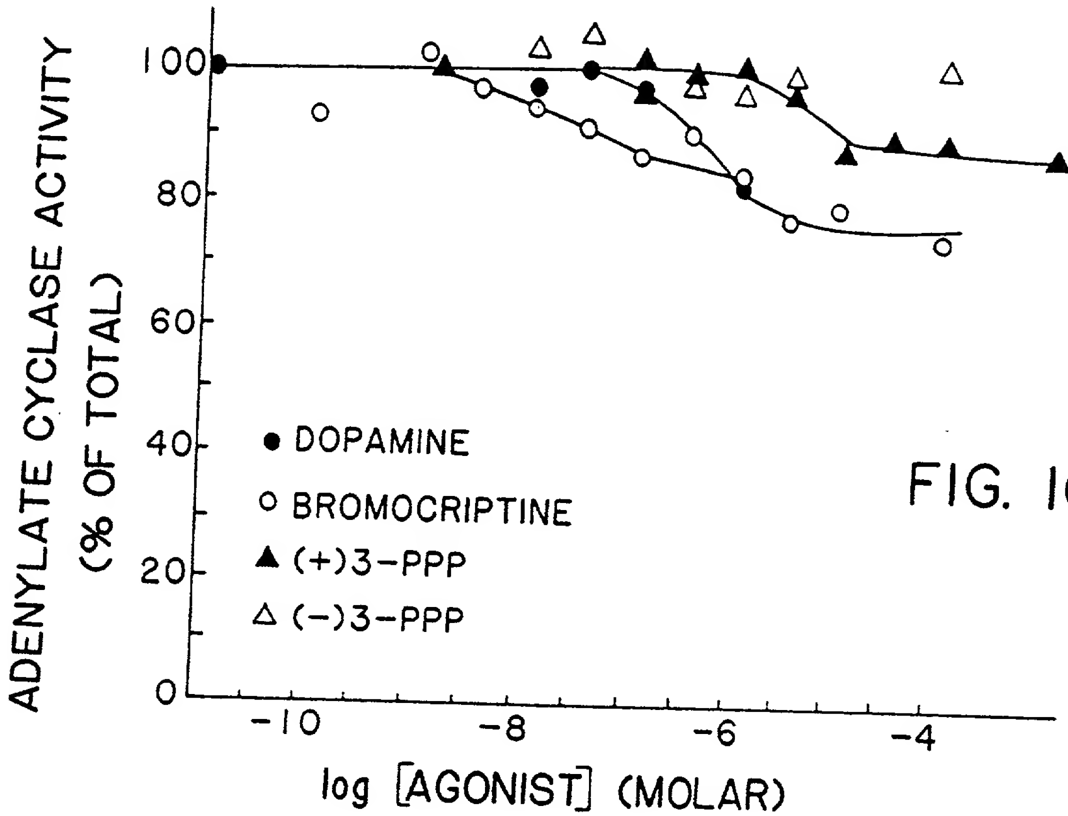


FIG. 10A

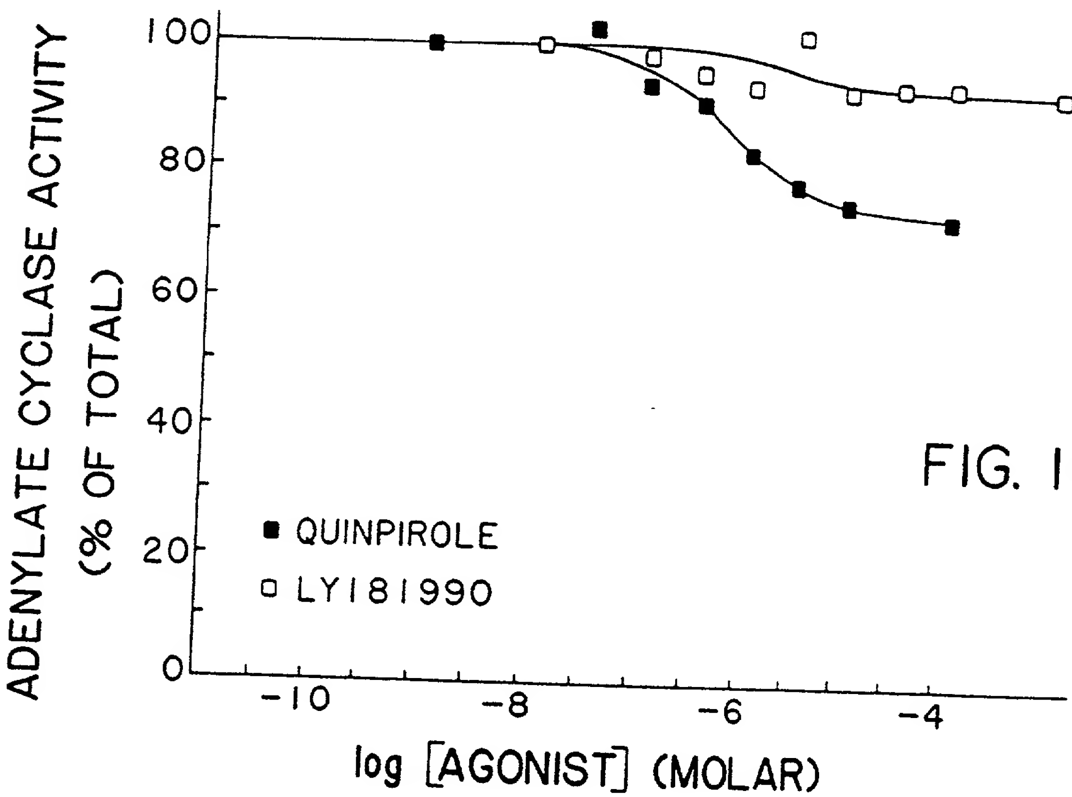


FIG. 10B

FIG. 12A

	CONTROL			+P.T.		
	BASAL	FSK	FSK+DA	BASAL	FSK	FSK+DA
$\bar{X}$	2.1	22.6	14.3	1.7	26.7	23.1
S.E.	0.2	2.2	2.1	0.4	2.0	0.5
INH	—	—	41%	—	—	14%

FIG. 12B

	CONTROL				+P.T.			
	BASAL	VIP	DA	VIP+DA	BASAL	VIP	DA	VIP+DA
$\bar{X}$	0.60	2.41	0.32	0.84	0.61	2.68	0.55	2.56
S.E.	0.02	0.31	0.02	0.13	0.09	0.08	0.03	0.25
INH	—	—	53%	71%	—	—	10%	3%

FIG. 12C

	CONTROL				+P.T.			
	BASAL	VIP	DA	VIP+DA	BASAL	VIP	DA	VIP+DA
$\bar{X}$	0.78	5.1	0.25	0.76	0.64	5.29	0.66	4.76
S.E.	0.04	0.4	0.03	0.01	0.01	0.44	0.03	0.16
INH	—	—	68%	88%	—	—	0%	12%

FIG. 13B-1

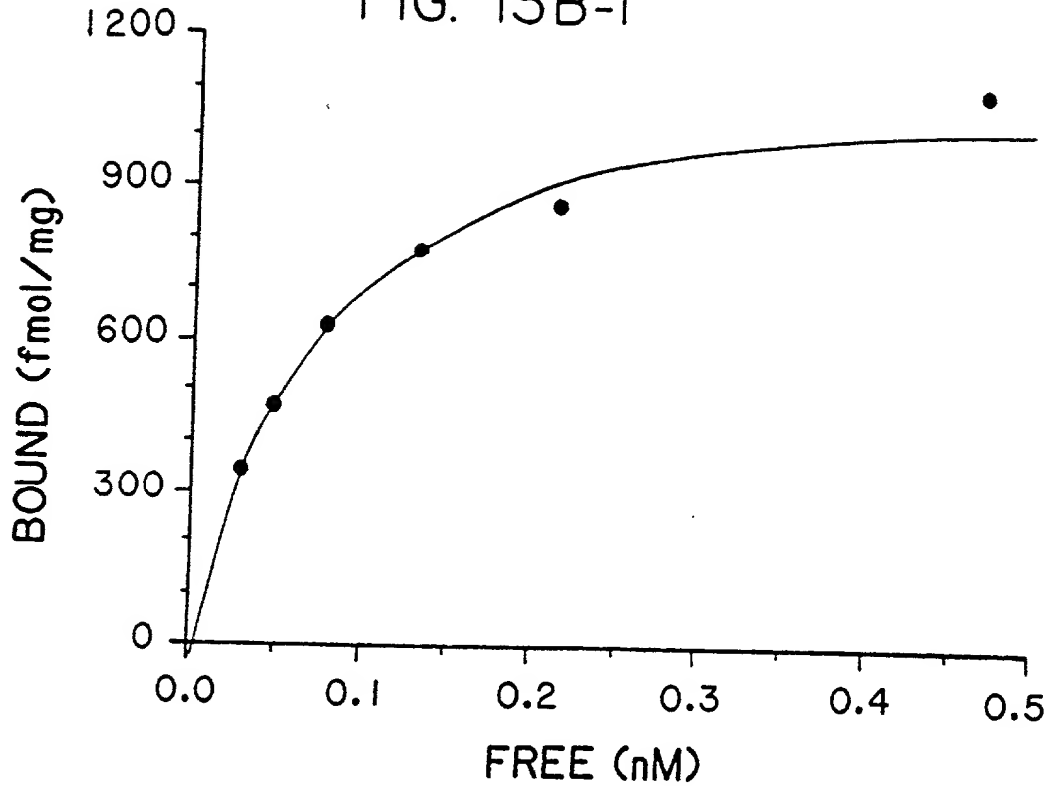


FIG. 13B-2

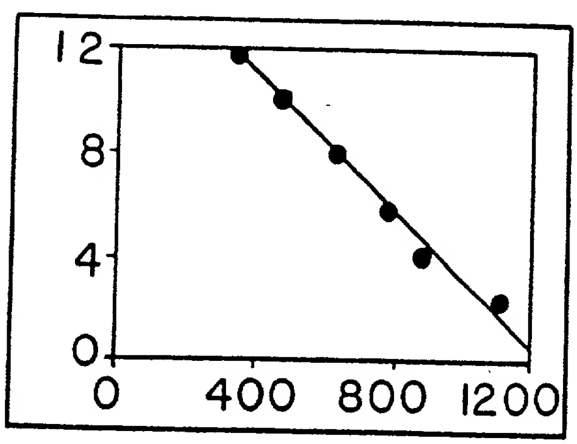
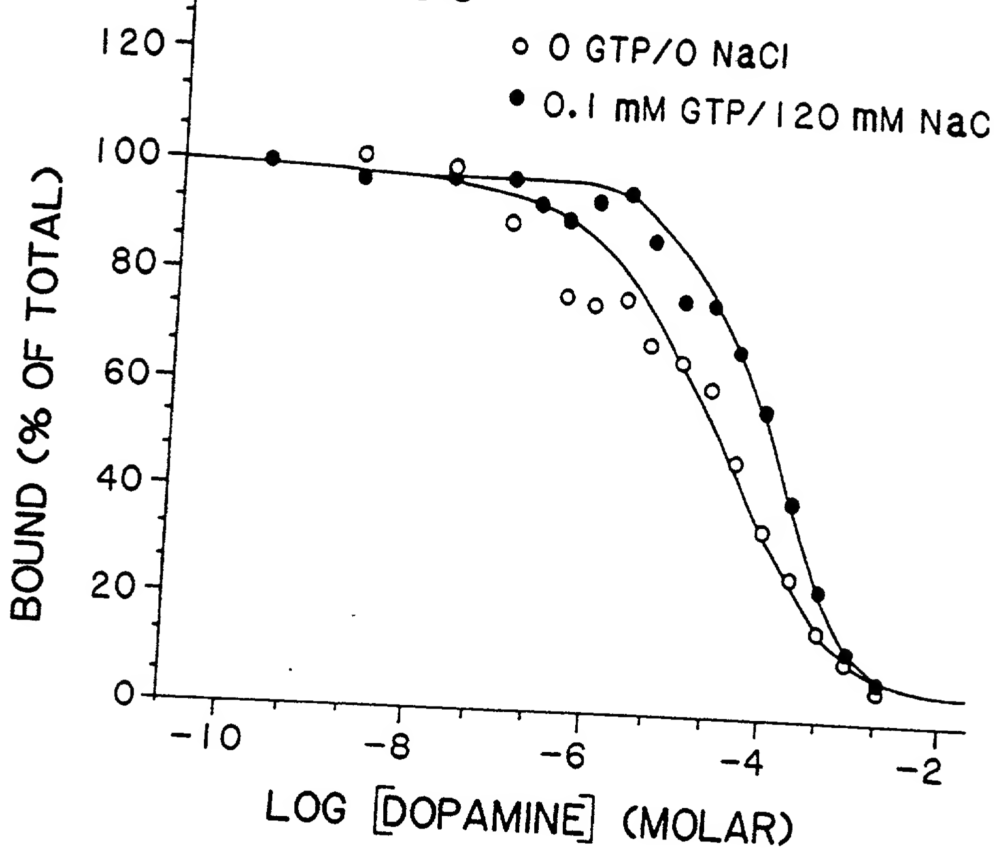


FIG. 13C



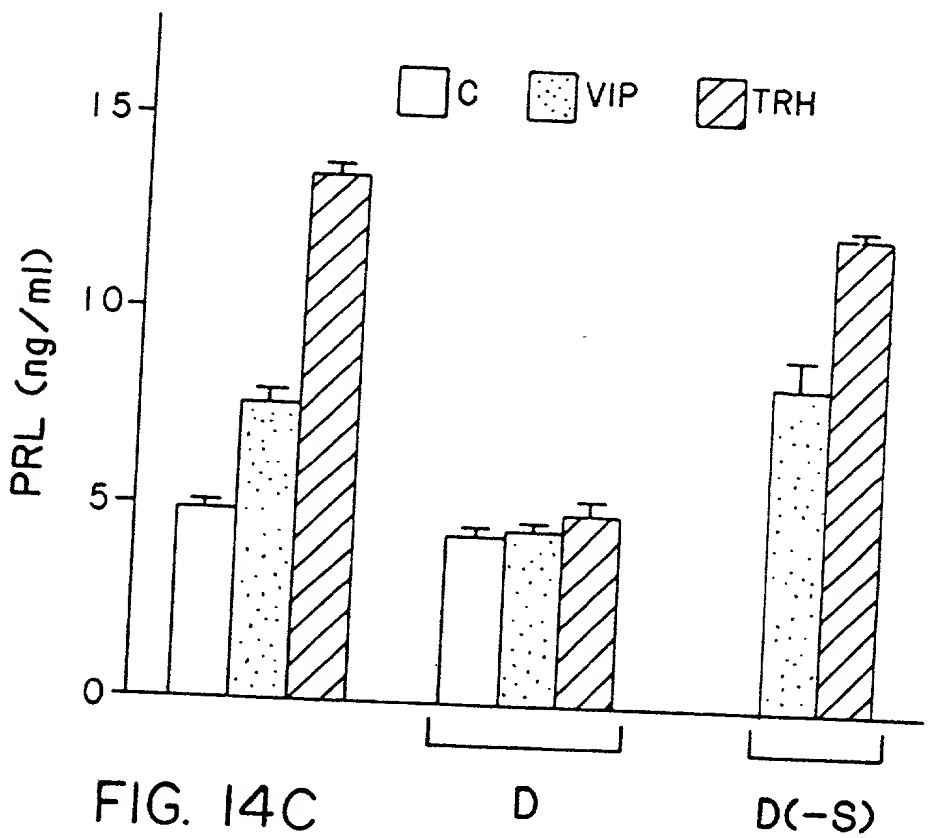


FIG. 14C

FIG.14A

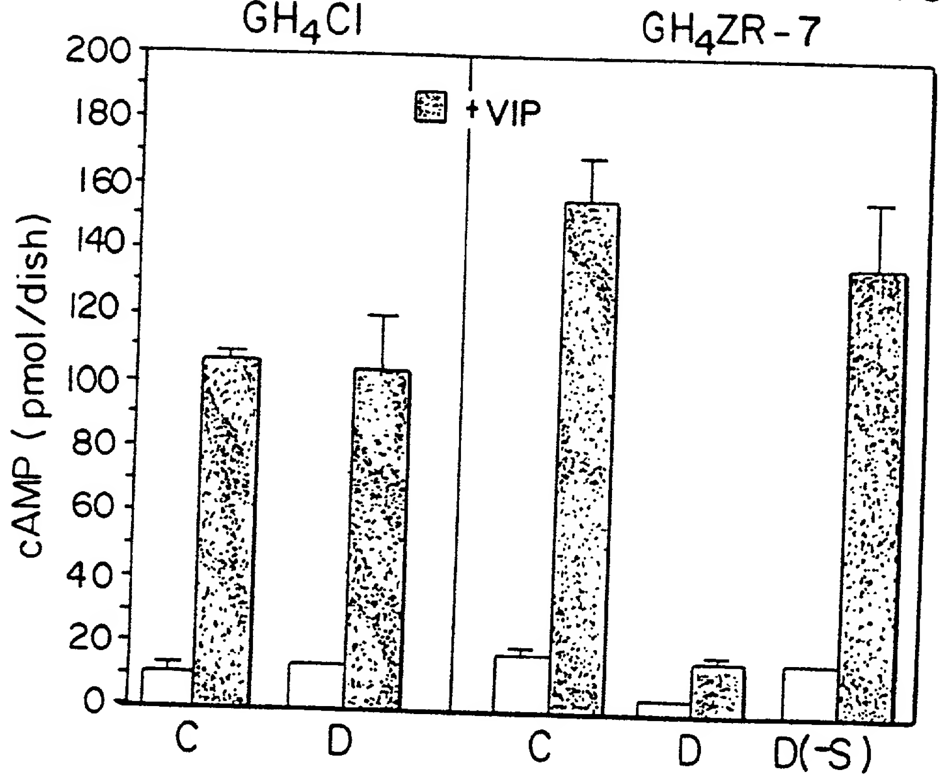
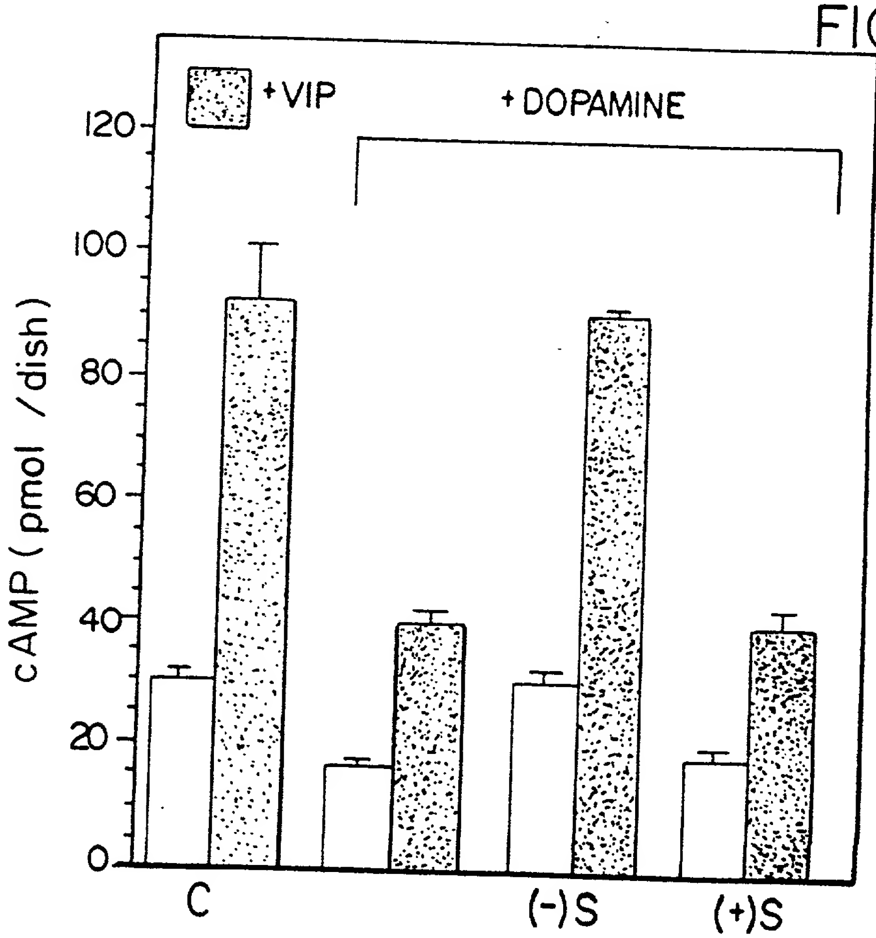


FIG.14B



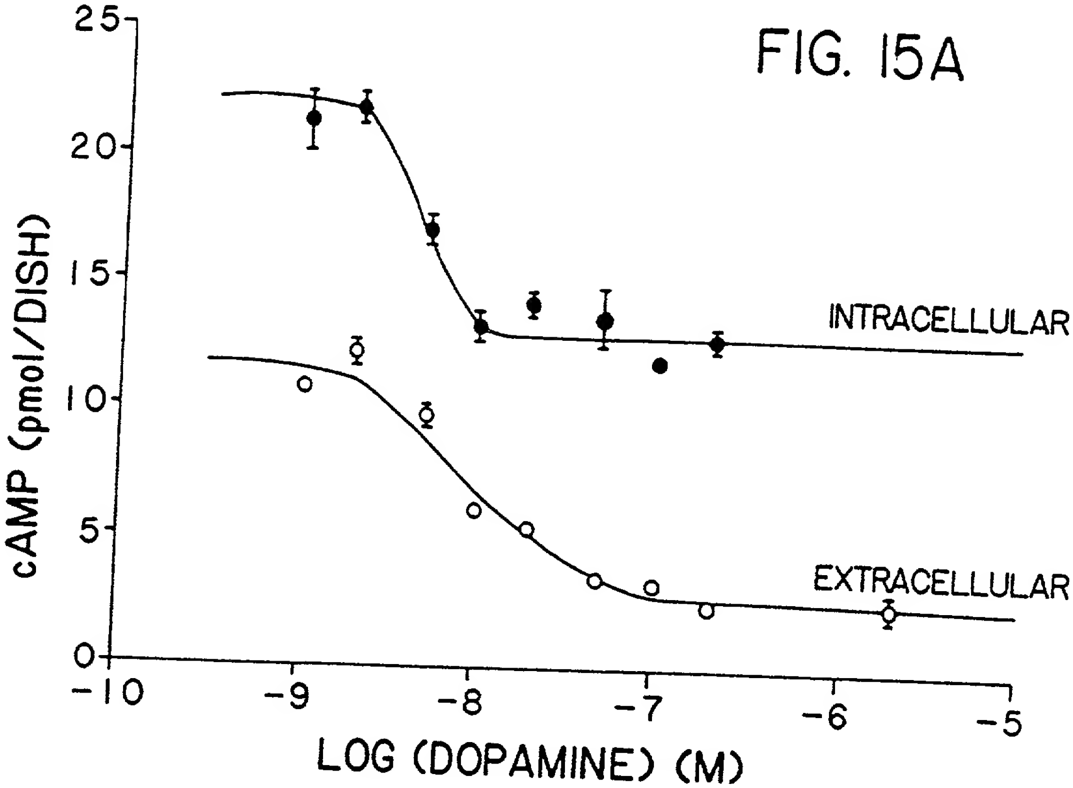


FIG. 15A

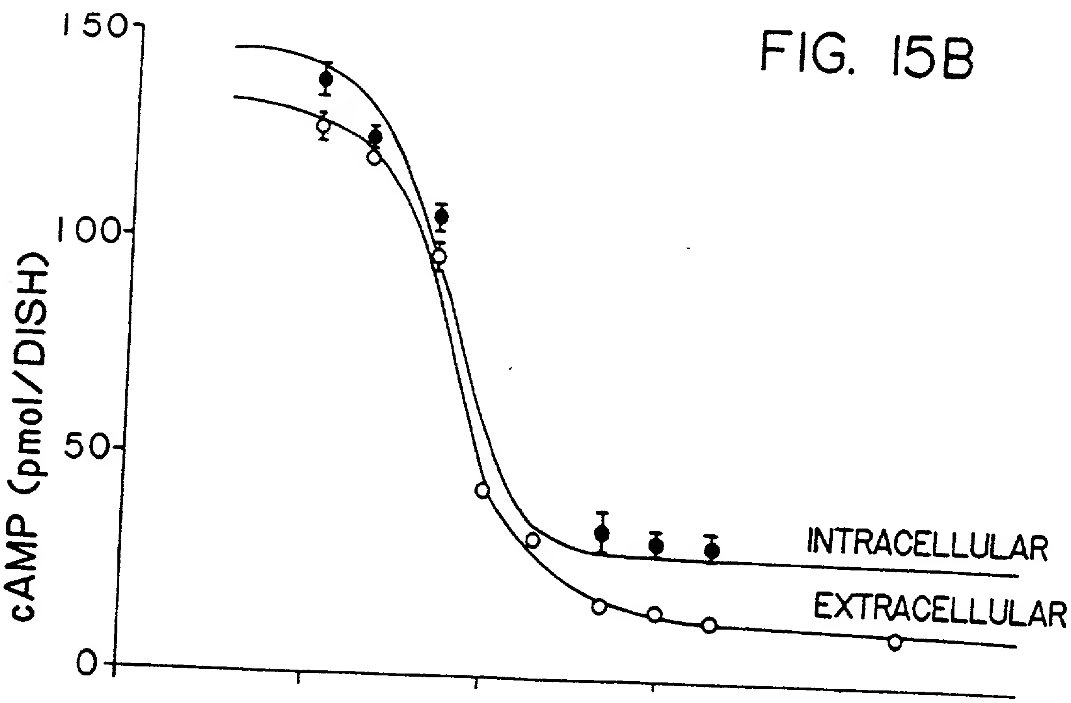


FIG. 15B

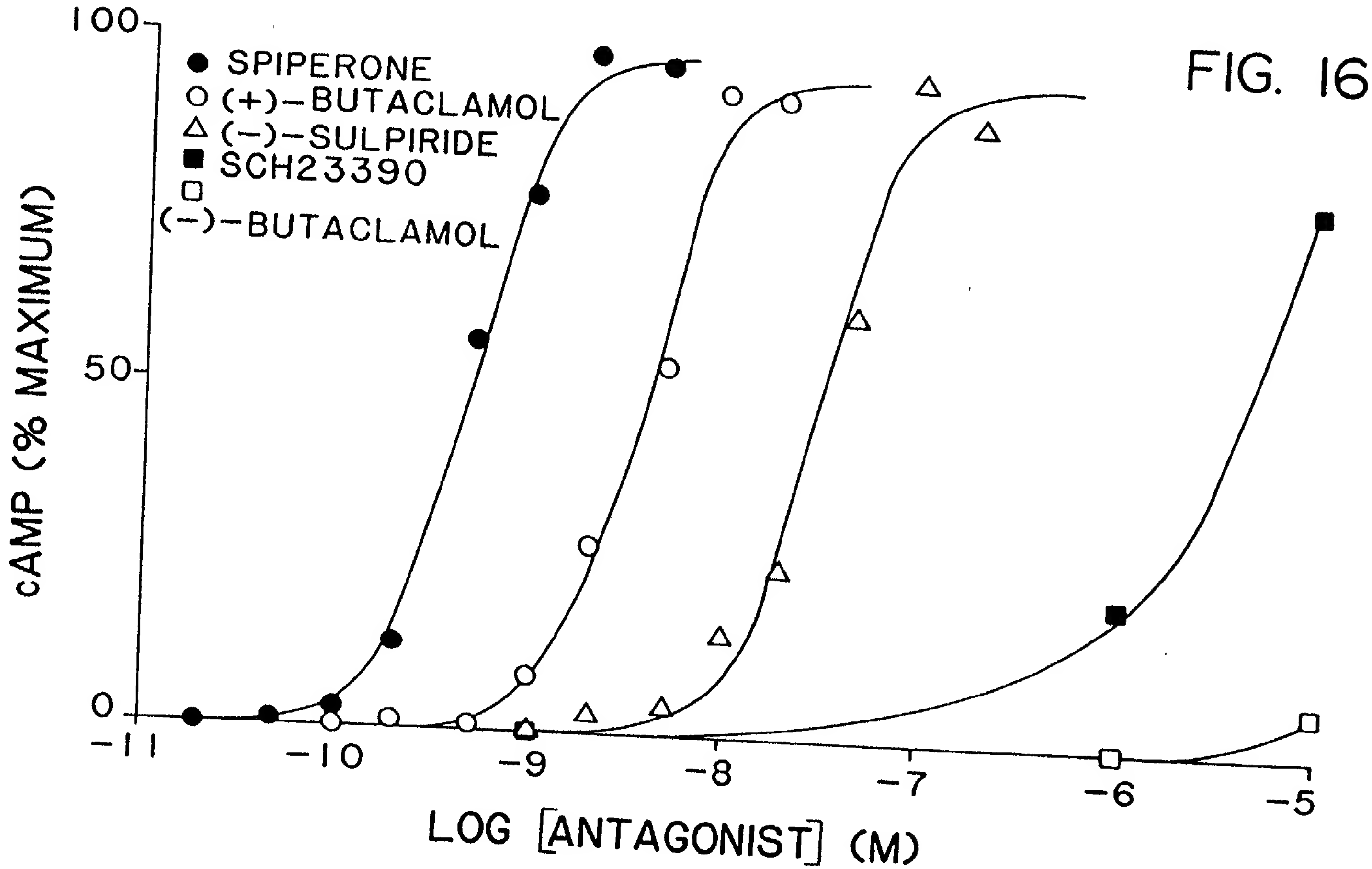

SPIPERONE
(+)-BUTACLAMOL
(-)-SULPIRIDE
SCH23390
(-)-BUTACLAMOL
100
50
0
cAMP (% MAXIMUM)
-11
-10
-9
-8
-7
-6
-5
LOG [ANTAGONIST] (M)

FIG. 16

FIG.17A

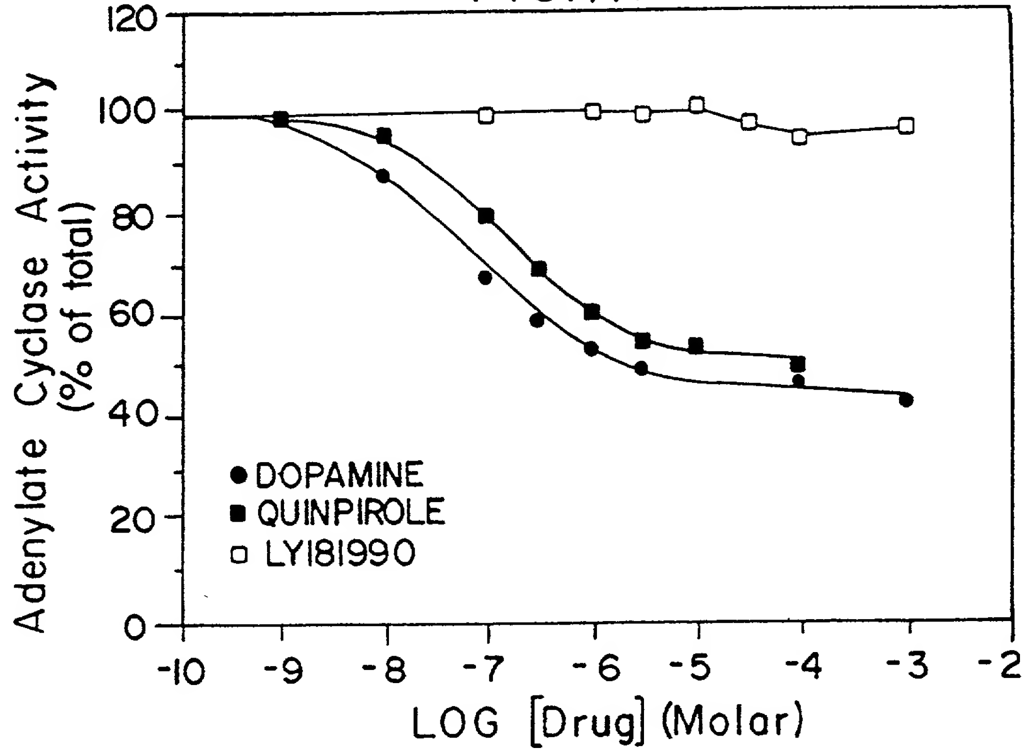
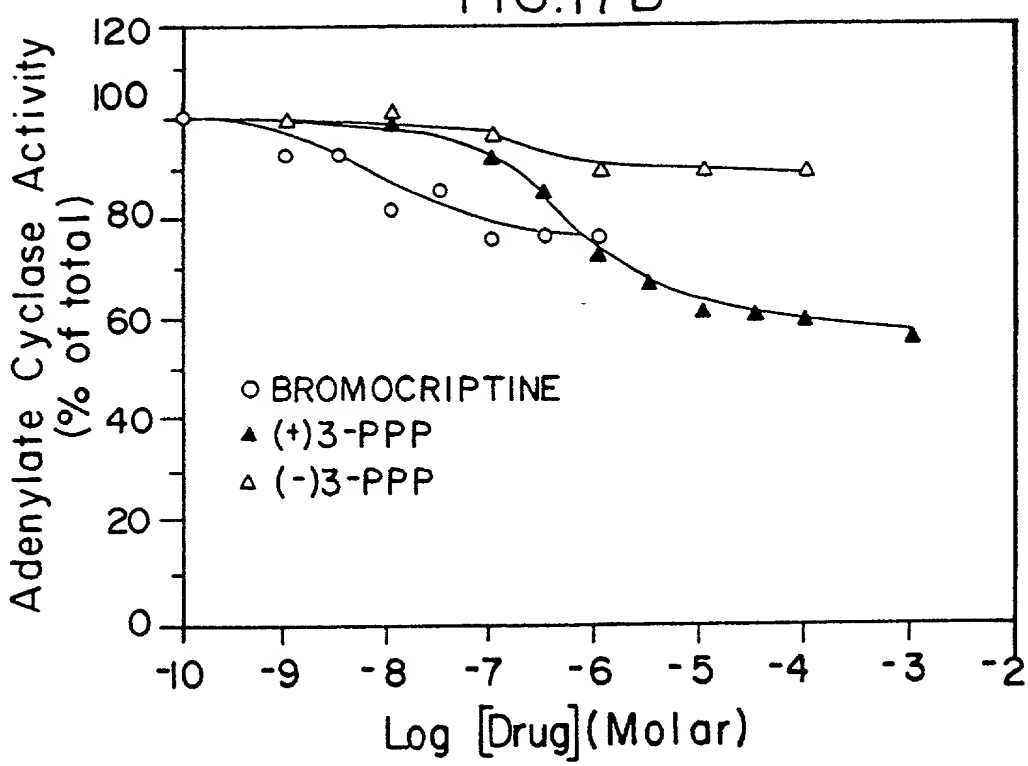


FIG.17B



```
-33 AGAGCCTGGCCACCCAGTGGCTCCACCGCCCTG

                 *              10                             *          20
METAspProLeuAsnLeuSerTrpTyrAspAspAspLeuGluArgGlnAsnTrpSerArg
ATGGATCCACTGAATCTGTCCTGGTATGATGATGATCTGGAGAGGCAGAACTGGAGCCGG
|||||||||||||| ||||||||||| ||||| |||||||||||||||||||||||||||
ATGGATCCACTGAACCTGTCCTGGTACGATGACGATCTGGAGAGGCAGAACTGGAGCCGG

      *                         30                                    40
ProPheAsnGlySerAspGlyLysAlaAspArgProHisTyrAsnTyrTyrAlaThrLeu
CCCTTCAACGGGTCAGACGGGAAGGCGGACAGACCCCACTACAACTACTATGCCACACTG
|||||||| |||||||| |||||||| ||||| ||||||||||||||||||||||  |||   120
CCCTTCAATGGGTCAGAAGGGAAGGCAGACAGGCCCCACTACAACTACTATGCCATGCTG
                 Glu                                   MET
```

FIG. 18A

```
                |                       50                           60
LeuThrLeuLeuIleAlaValIleValPheGlyAsnValLeuValCysMETAlaValSer
CTCACCCTGCTCATCGCTGTCATCGTCTTCGGCAACGTGCTGGTGTGCATGGCTGTGTCC
|||||||| ||||||  | |||||||||| ||||| |||||||||||||||||||| |||
CTCACCCTCCTCATCTTTATCATCGTCTTTGGCAATGTGCTGGTGTGCATGGCTGTATCC
               PheIle

                                  70                       ||        80
ArgGluLysAlaLeuGlnThrThrThrAsnTyrLeuIleValSerLeuAlaValAlaAsp
CGCGAGAAGGCGCTGCAGACCACCACCAACTACCTGATCGTCAGCCTCGCAGTGGCCGAC
|| ||||||||  |||||||||||||||||||| |||| |||||||| || ||||| ||      240
CGAGAGAAGGCTTTGCAGACCACCACCAACTACTTGATAGTCAGCCTTGCTGTGGCTGAT

                                  90                         100
LeuLeuValAlaThrLeuValMETProTrpValValTyrLeuGluValValGlyGluTrp
                                             ▼
CTCCTCGTCGCCACACTGGTCATGCCCTGGGTTGTCTACCTGGAGGTGGTAGGTGAGTGG
|| || || ||||||||||| ||||| ||||||||||||||||||||||| |||||||||
CTTCTGGTGGCCACACTGGTAATGCCGTGGGTTGTCTACCTGGAGGTGGTGGGTGAGTGG
```

FIG. 18B

TOT280 " 85E4E660

```
                                 110                             |||      120
LysPheSerArgIleHisCysAspIlePheValThrLeuAspValMETMETCysThrAla
         .         .         .         .         .         .
AAATTCAGCAGGATTCACTGTGACATCTTCGTCACTCTGGACGTCATGATGTGCACGGCG
||||||||||||||||||||||||||||| ||||||||||| |||||||||||||| ||        360
AAATTCAGCAGGATTCACTGTGACATCTTTGTCACTCTGGATGTCATGATGTGCACAGCA

                           130                           140
SerIleLeuAsnLeuCysAlaIleSerIleAspArgTyrThrAlaValAlaMETProMET
         .         .         .    ▼    .         .         .
AGCATCCTGAACTTGTGTGCCATCAGCATCGACAGGTACACAGCTGTGGCCATGCCCATG
|||||||||||| |||||||||||||||| |||||||||||||||||||| |||||||||
AGCATCCTGAACCTGTGTGCCATCAGCATTGACAGGTACACAGCTGTGGCAATGCCCATG

                           150                           160
LeuTyrAsnThrArgTyrSerSerLysArgArgValThrValMETIleSerIleValTrp
         .         .         .         .         .         .
CTGTACAATACGCGCTACAGCTCCAAGCGCCGGGTCACCGTCATGATCTCCATCGTCTGG
||||| || || |||||||||||||||||||| || || ||||||||  |||| ||||||       480
CTGTATAACACACGCTACAGCTCCAAGCGCCGAGTTACTGTCATGATTGCCATTGTCTGG
                                                     Ala
```

FIG. 18C

```
                 IV                             170                            180
ValLeuSerPheThrIleSerCysProLeuLeuPheGlyLeuAsnAsnAlaAspGlnAsn
GTCCTGTCCTTCACCATCTCCTGCCCACTCCTCTTCGGACTCAATAACGCAGACCAGAAC
||||||||||||||||||||||||||||| |||||||||||||| ||  |||||||||| 
GTCCTGTCCTTCACCATCTCCTGCCCACTGCTCTTCGGACTCAACAATACAGACCAGAAT
                                                    Thr

                                   190          V              200
GluCysIleIleAlaAsnProAlaPheValValTyrSerSerIleValSerPheTyrVal
GAGTGCATCATTGCCAACCCGGCCTTCGTGGTCTACTCCTCCATCGTCTCCTTCTACGTG
||||| |||||||||||||| ||||| ||||||||||||||||| ||||| |||||||||   600
GAGTGTATCATTGCCAACCCTGCCTTTGTGGTCTACTCCTCCATTGTCTCATTCTACGTG

                                   210                        220
ProPheIleValThrLeuLeuValTyrIleLysIleTyrIleValLeuArgArgArgArg
CCCTTCATTGTCACCCTGCTGGTCTACATCAAGATCTACATTGTCCTCCGCAGACGCCGC
!||||||| ||||| ||||||||||| ||||| |||||||| |||||||| |  ||||| 
CCCTTCATCGTCACTCTGCTGGTCTATATCAAAATCTACATCGTCCTCCGGAAGCGCCGG
                                                      Lys
```

FIG. 18D

09934358.082101

```
                         230                 240
LysArgValAsnThrLysArgSerSerArgAlaPheArgAlaHisLeuArgAlaProLeu
         .         .         .         .         .         .
AAGCGAGTCAACACCAAACGCAGCAGCCGAGCTTTCAGGGCCCACCTGAGGGCTCCACTA
||||| |||||||||||| ||||||||| ||||||||||| ||| |||||| | | |||||    720
AAGCGGGTCAACACCAAGCGCAGCAGTCGAGCTTTCAGAGCCAACCTGAAGACACCACTC
                                            Asn   LysThr

      *                  250                                 *
LysGlyAsnCysThrHisProGluAspMETLysLeuCysThrValIleMETLysSerAsn
  ▼      .         .         .         .         .         .
AAGGGCAACTGTACTCACCCCGAGGACATGAAACTCTGCACCGTTATCATGAAGTCTAAT
!!!
AAG.........................................................

                         270                 280
GlySerPheProValAsnArgArgArgValGluAlaAlaArgArgAlaGlnGluLeuGlu
         .         .         ▼         .         .         .
GGGAGTTTCCCAGTGAACAGGCGGAGAGTGGAGGCTGCCCGGCGAGCCCAGGAGCTGGAG
                              || |||||||| ||||| |||||||||||
..............................GATGCTGCCCGCCGAGCTCAGGAGCTGGAA    840
                              Asp
```

FIG. 18E

```
                           290                           300
METGluMETLeuSerSerThrSerProProGluArgThrArgTyrSerProIleProPro
         .         .         .         .         .         .
ATGGAGATGCTCTCCAGCACCAGCCCACCCGAGAGGACCCGGTACAGCCCCATCCCACCC
||||||||||| || ||||||||||| || |||||||||||||| ||||||||||| |||
ATGGAGATGCTGTCAAGCACCAGCCCCCCAGAGAGGACCCGGTATAGCCCCATCCCTCCC

                           310                           320
SerHisHisGlnLeuThrLeuProAspProSerHisHisGlyLeuHisSerThrProAsp
         .         .         .         .         .         .
AGCCACCACCAGCTGACTCTCCCCGACCCGTCCCACCATGGTCTCCACAGCACTCCCGAC
|| ||||||||||| |||||||| || || |||||||| || || || |||| ||| |||   960
AGTCACCACCAGCTCACTCTCCCTGATCCATCCCACCACGGCCTACATAGCAACCCTGAC
                                                   Asn

                           330                           339
SerProAlaLysProGluLysAsnGlyHisAlaLys   AspHisProLysIleAlaLys
         .         .         .            .         .
AGCCCCGCCAAACCAGAGAAGAATGGGCATGCCAAA...GACCACCCCAAGATTGCCAAG
|| || ||||||||||||||||||||||| |||||    | | | |||| ||||||||||
AGTCCTGCCAAACCAGAGAAGAATGGGCACGCCAAGATTGTCAATCCCAGGATTGCCAAG
                                    IleValAsn   Arg
```

FIG. 18F

```
                                  349                                        359
IlePheGluIleGlnThrMETProAsnGlyLysThrArgThrSerLeuLysThrMETSer
.        .         .         .         .         .
ATCTTTGAGATCCAGACCATGCCCAATGGCAAAACCCGGACCTCCCTCAAGACCATGAGC
 |||||||||||||||||||||||||||||||||||||||||||||| ||||| ||||||  1077
TTCTTTGAGATCCAGACCATGCCCAATGGCAAAACCCGGACCTCCCTTAAGACGATGAGC
Phe

                                  369                                        379
ArgArgLysLeuSerGlnGlnLysGluLysLysAlaThrGln[METLeuAlaIleValLeu]
.        .         .         .         .         .
CGTAGGAAGCTCTCCCAGCAGAAGGAGAAGAAAGCCACTCAGATGCTCGCCATTGTTCTC
|| || ||||||||||||||||||||||||||||||||||||||||| ||||||||||||
CGCAGAAAGCTCTCCCAGCAGAAGGAGAAGAAAGCCACTCAGATGCTTGCCATTGTTCTC

                      VI
                                  389                                        399
[GlyValPheIleIleCysTr0LeuProPhePheIleThrHisIleLeuAsnIle]HisCys
▼        .         .         .         .         .
GGCGTGTTCATCATCTGCTGGCTGCCCTTCTTCATCACACACATCCTGAACATACACTGT
|| |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||  1197
GCCGTCAACCCCATCATCTACACCACCTTCAACATCGAGTTCCGCAAGGCCTTCATGAAG
                                                     MET
```

FIG. 18G

09934358.082101

```
                         409                                   VII  419
AspCysAsnIleProPro[ValLeuTyrSerAlaPheThrTrpLeuGlyTyrValAsnSer

GACTGCAACATCCCGCCTGTCCTGTACAGCGCCTTCACGTGGCTGGGCTATGTCAACAGC
|| |||||||||| || ||||| |||||||||||||| ||||||||||||||||||||| 
GATTGCAACATCCCACCAGTCCTCTACAGCGCCTTCACATGGCTGGGCTATGTCAACAGT

                           429                                    439
AlaValAsnProIleIleTyrThrThrPhe]AsnIleGluPheArgLysAlaPheLeuLys

GCCGTGAACCCCATCATCTACACCACCTTCAACATTGAGTTCCGCAAGGCCTTCCTGAAG
||||| ||||||||||||||||||||||||||||| ||||||||||||||||||| |||||  1317
GCCGTCAACCCCATCATCTACACCACCTTCAACATCGAGTTCCGCAAGGCCTTCATGAAG
                                                       MET
IleLeuHisCys *

ATCCTCCACTGCTGACTCTGCTGCCTGCCCGCACAGCAGCCTGCTTCCCACCTCCCTGCC
||| | ||||||||||
ATCTTGCACTGCTGA
```

FIG. 18H

TOT280"8SEhE660

CAGGCCGGCCAGCCTCACCCTTGCGAACCGTGAGCAGGAAGGCCTGGGTGGATCGGCCTC 1437
CTCTTCTTAGCCCCGGCAGGCCCTGCAGTGTTCGCTTGGCTCCATGCTCCTCACTGCCCG
CACACCCTCACTCTGCCAGGGCAGTGCTAGTGAGCTGGGCATGGTACCAGCCCTGGGGCT 1557
GGCCCCAGCTCAGGGGCAGCTCATAGAGTCCCCCCTCCCACCTCCAGTCCCCCTATCCTT
GGCACCAAAGATGCAGCCGCCTTCCTTGACCTTCCTCTGGGGCTCTAGGGTTGCTGGAGC 1677
CTGAGTCAGGGCCCAGAGGCTGAGTTTTCTCTTTGTGGGGCTTGGCGTGGAGCAGGCGGT
GGGGAGAGATGGACAGTTCACACCCTGCAAGGCCCACAGGAGGCAAGCAAGCTCTCTTGC 1797
CGAGGAGCCAGGCAACTTCAGTCCTGGGAGACCCATGTAAATACCAGACTGCAGGTTGGA
CCCCAAGGATTCCCAAGCCAAAAACCTTAGCTCCCTCCCGCACCCCGATGTGGACCTCTA 1917

FIG. 18I

09934358.082101

CTTTCCAGGCTAGTCCGGACCCACCTCACCCCGTTACAGCTCCCCAAGTGGTTTCCACAT

GCTCTGAGAAGAGGAGCCCTCATCTTGAAGGGCCCAGGAGGGTCTATGGGAGAGGAACT 2037

CCTTGGCCTAGCCCACCCTGCTGCCTTCTGACGGCCCTGCAATGTATCCCTTCTCACAGC

ACATGCTGGCCAGCCTGGGGCCTGGCAGGGAGGTCAGGCCCTGGAACTCTATCTGGGCCT 2157

GGGCTAGGGACATCAGAGGTTCTTTGAGGGACTGCCTCTGCCACACTCTGACGCAAAACC

ACTTTCCTTTTCTATTCCTTCTGGCCTTTCCTCTCTCCTGTTTCCCTTCCCTTCCACTGC 2277

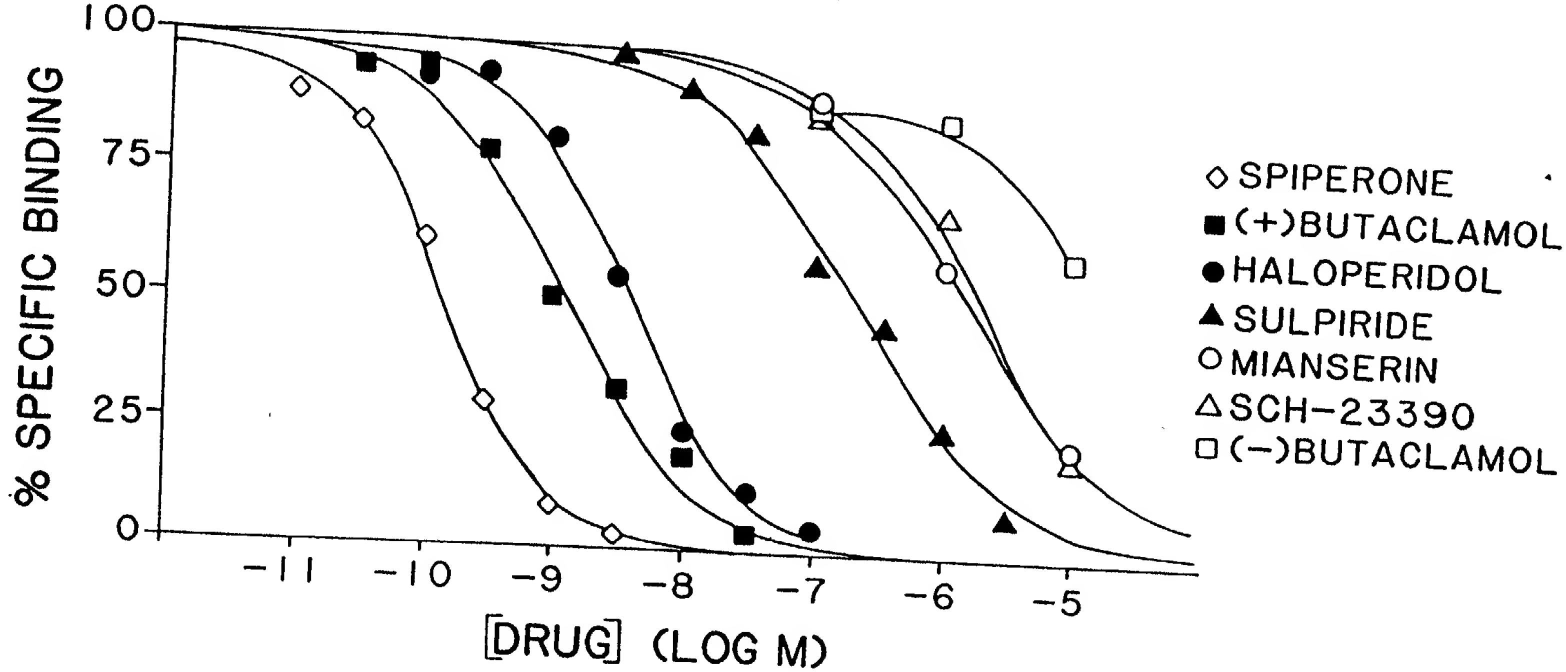
CTCTGCCTTAGAGGAGCCCACGGCTAAGAGGCTGCTGAAAACCATCTGGCCTGGCCTGGC

CCTGCCCTGAGGAAGGAGGGCAAGCTGCAGCTTGGGAGAGCCCCTGGGGCCTAGACTCTG 2397

TAACATCACTATCCGATGCACCAAACTAATAAACTTTGACGAGTCACCTTC $(A)_n$ 2449

FIG. 18J

FIG. 19


% SPECIFIC BINDING
100
75
50
25
0
−11
−10
−9
−8
−7
−6
−5
[DRUG] (LOG M)
◇ SPIPERONE
■ (+)BUTACLAMOL
● HALOPERIDOL
▲ SULPIRIDE
○ MIANSERIN
△ SCH-23390
□ (−)BUTACLAMOL

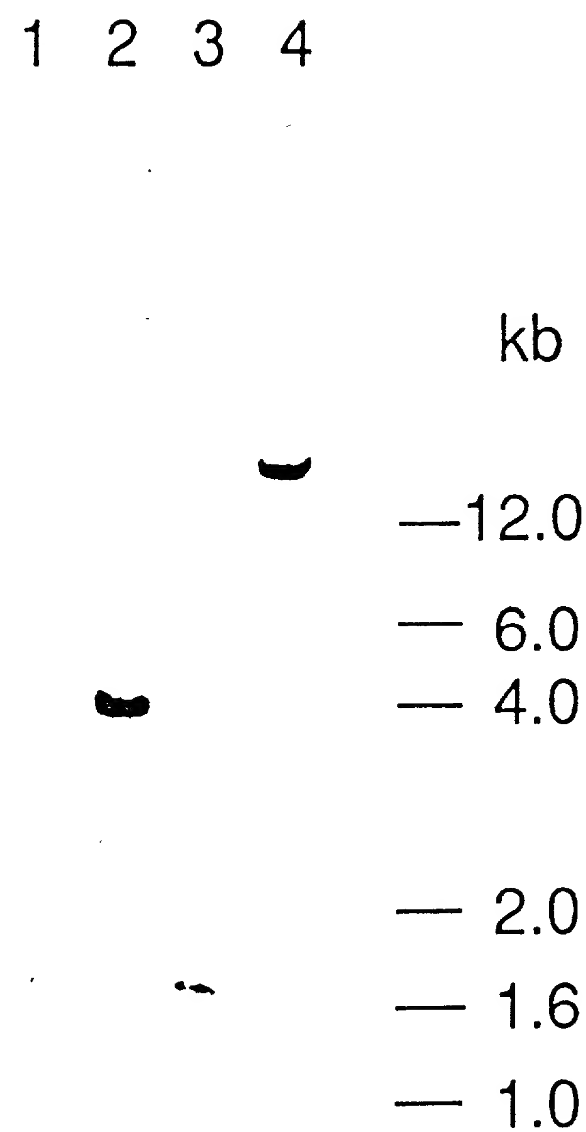
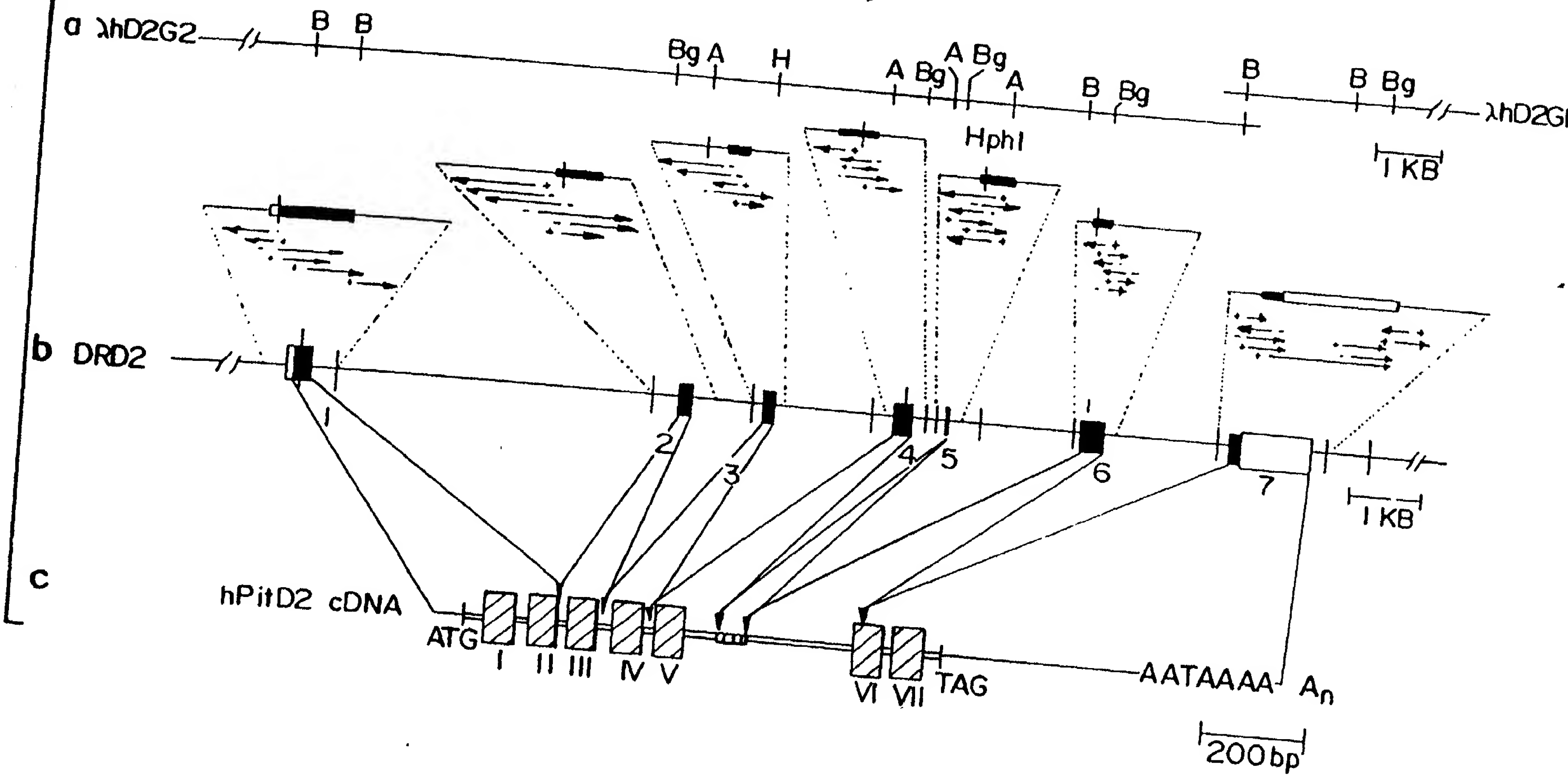


FIG. 20

FIG. 21



a λhD2G2
B
B
Bg
A
H
A
Bg
A
Bg
A
HphI
B
Bg
B
B
Bg
λhD2G1
1 KB
b DRD2
1
2
3
4
5
6
7
1 KB
c
hPitD2 cDNA
ATG
I
II
III
IV
V
VI
VII
TAG
AATAAAA
A_n
200bp

DRUG	HUMAN D_2	RAT D_2	RAT STRIATUM
SPIPERONE	0.125	0.35	0.56
(+) BUTACLAMOL	0.94	1.2	1.6
HALOPERIDOL	2.4	5.1	5.8
SULPIRIDE	206	160	205
MIANSERIN (5-HT)	2685	4300	4600
SCH 23390 (D1)	2145	2500	3300
(+) BUTACLAMOL	>10,000	>10,000	>10,000
Kd [^{3}H] DOMPERIDONE	0.74	0.40	0.40

FIG. 22

FIG. 23

	285[1]	286
exon1...GGAGgtaggtg...intron1...tccccagGTGG...exon2		
	395	396
exon2...ACAGgtgagcc...intron2...cttgcagGTAC...exon3		
	532	533
exon3...GCAGgtacatt...intron3...cccccagACCA...exon4		
	723	724
exon4...AAAGgtctcaa...intron4...tccacagGGCA...exon5		
	810	811
exon5...AGTGgtaagtg...intron5...ggtgcagGAGG...exon6		
	1138	1139
exon6...CTCGgtgagtc...intron6...cccccagGCGT...exon7		

[1] Numbering begins with A of the putative initiator methionine codon (see Fig. 18)